Accession	pgID	Master Protein	Description (curated)	Length	Localization (SC)	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	ENV SC	STR SC	THY SC	Total SC	Function (putative)	MapMan Bin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AT1G01080	1	AT1G01080.1	33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative	293	STR		9.0	32.57	0.0	100.0	0.0	26.0		27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT1G01090	2	AT1G01090.1	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring)	428	ENV-STR	Ch/E/IM	7.16	47.17	55.685150490732 2	40.192614001028 6	4.1222355082391 8	60.0	metabolism lipid	11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	chloroplast	Y	C	envelope-inner-peripheral-stromal-side	
AT1G01620	3	AT1G01620.1	PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3); water channel	286	ENV	other	9.01	30.63	100.0	0.0	0.0	6.0	transporter aquaporin	34.19.1 transport.Major Intrinsic Proteins.PIP	other (e.g. cytoplasm)			plasma membrane	6.0
AT1G01790	4	AT1G01790.1	KEA1 (K EFFLUX ANTIPORTER 1); potassium:hydrogen antiporter	618	ENV	Ch/E ?	6.1	64.98	100.0	0.0	0.0	126.0	transporter K	34.8 transport.metabolite transporters at the envelope membrane	undefined			envelope-inner-integral	13.0
AT1G02150	5	AT1G02150.1	pentatricopeptide (PPR) repeat-containing protein	524			8.23	59.88	0.0	100.0	0.0	6.0		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	undefined	Y	M	-	

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AT1G02280	6	AT1G02280.1	TOC33 (PLASTID PROTEIN IMPORT 1); GTP binding	297	ENV	Ch/E/OM	9.1	32.92	91.818322563681 6	0.0	8.1816774363183 6	64.0	protein targeting Toc	29.3.3 protein.targeting.chloroplast	undefined			envelope-outer-integral	
AT1G02560	7	AT1G02560.1	CLPP5 (NUCLEAR ENCODED CLP PROTEASE 1); endopeptidase Clp	298	STR-ENV	Ch/E & Ch/S	8.34	32.35	42.222937711429 2	57.777062288570 8	0.0	69.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-inner-peripheral-stromal-side	
AT1G02910	8	AT1G02910.1	LPA1 (LOW PSII ACCUMULATION1); binding	453			9.37	50.74	0.0	0.0	100.0	5.0		29.8 protein assembly and cofactor ligation	chloroplast	Y	C	thylakoid-integral	2.0
AT1G03130	9	AT1G03130.1	PSAD-2 (photosystem I subunit D-2)	204	THY-ENV	Ch/Th	9.78	22.3	21.024468402902 9	0.173049512088748	78.802482085008 4	401.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT1G03310	10	AT1G03310.1	ATISA2/BE2/DBE1/ISA2 (DEBRANCHING ENZYME 1); alpha-amylase/isoamylase	882			5.64	98.88	0.0	100.0	0.0	2.0		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	chloroplast	Y	C	plastid	
AT1G03475	11	AT1G03475.1	LIN2 (LESION INITIATION 2); coproporphyrinogen oxidase	362	STR	Ch/S	7.66	40.76	6.5880350618345 3	93.411964938165 5	0.0	194.0	metabolism vitamin and pigment	19.8 tetrapyrrole synthesis.coproporphyrinogen III oxidase	chloroplast	Y	C	plastid stroma	

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AT1G03600	12	AT1G03600.1	photosystem II family protein	174	THY	Ch/Th/Lum	9.88	18.83	5.6049825868909 2	0.0	94.395017413109 1	59.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT1G03630	13	AT1G03630.1	POR C (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE); NADPH dehydrogenase/ oxidoreductase/ protochlorophyllide reductase	401	ENV-THY	Ch/E & Ch/Th	9.18	43.88	66.855847407684 8	1.6789604583651 4	31.46519213395	287.0	metabolism vitamin and pigment	19.14 tetrapyrrole synthesis.protochlorophyllide reductase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT1G03680	14	AT1G03680.1	ATHM1 (Arabidopsis thioredoxin M-type 1); thiol-disulfide exchange intermediate	179	STR-ENV	Ch	9.13	19.66	17.008956640770 4	82.991043359229 6	0.0	93.0	redox	21.1 redox.thioredoxin	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT1G03830	15	AT1G03830.1	guanylate-binding family protein	991			5.57	112.5	0.0	0.0	100.0	3.0		35.1 not assigned.no ontology	other (e.g. cytoplasm)			-	
AT1G04270	16	AT1G04270.1	RPS15 (CYTOSOLIC RIBOSOMAL PROTEIN S15); structural constituent of ribosome	152	ENV	Ch/E & other	10.34	17.13	100.0	0.0	0.0	1.0	translation cytosol	29.2.1.2.1.15 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S15	other (e.g. cytoplasm)			cytosol	

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AT1G04410	17	AT1G04410.1	malate dehydrogenase, cytosolic, putative	332	STR		6.1	35.57	0.0	100.0	0.0	39.0		8.2.9 TCA / org.transformation.other organic acid transformaitons.cytMDH	undefined			cytosol	
AT1G04420	18	AT1G04420.1	aldo/keto reductase family protein	412	STR		8.69	46.42	0.0	100.0	0.0	143.0		3.5 minor CHO metabolism.others	chloroplast	Y	C	plastid stroma	
AT1G04620	19	AT1G04620.1	coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family	462	THY-ENV	Ch/E & Ch/Th	8.36	51.66	43.799246953279 9	0.0	56.200753046720 1	7.0	redox ?	35.1 not assigned.no ontology	chloroplast	Y	C	-	
AT1G04820	20	AT1G04820.1	TUA4 (tubulin alpha-4 chain)	450	STR		4.92	49.54	0.0	100.0	0.0	12.0		31.1 cell.organisation	undefined			-	
AT1G05140	21	AT1G05140.1	membrane-associated zinc metalloprotease, putative	441			9.06	47.77	0.0	0.0	100.0	7.0		29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	-	4.0
AT1G05190	22	AT1G05190.1	EMB2394 (EMBRYO DEFECTIVE 2394); structural constituent of ribosome	223	STR-ENV	Ch/S	9.89	24.7	28.736942373205 8	71.263057626794 3	0.0	171.0	translation stroma	29.2.1.1.1.2.6 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L6	undefined	Y	C	plastid ribosome	

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AT1G06230	23	AT1G06230.1	GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding	766			5.23	84.09	0.0	100.0	0.0	3.0		27.3.52 RNA.regulation of transcription.Global transcription factor group	other (e.g. cytoplasm)			-	
AT1G06430	24	AT1G06430.1	FTSH8 (FtsH protease 8); ATP-dependent peptidase/ ATPase/ metallopeptidase/ zinc ion binding	685	THY	Ch/Th	5.71	73.19	6.3988350012596 5	0.0	93.601164998740 4	212.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	undefined	Y	C	thylakoid-integral	1.0
AT1G06680	25	AT1G06680.1	PSBP-1 (OXYGEN-EVOLVING ENHANCER PROTEIN 2); poly(U) binding	263	THY	Ch/Lum	6.9	28.09	4.2594653267745 5	9.6587749264324 6	86.081759746793	325.0	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT1G06690	26	AT1G06690.1	aldo/keto reductase family protein	377	ENV	Ch/E & Ch/Th	8.85	41.49	100.0	0.0	0.0	11.0	redox ?	35.1 not assigned. no ontology	undefined	Y	C	plastoglobules	
AT1G06820	27	AT1G06820.1	CRTISO (CAROTENOID ISOMERASE); carotenoid isomerase	595	ENV	Ch/E/IM	8.33	65.42	100.0	0.0	0.0	6.0	metabolism vitamin and pigment	16.1.4 secondary metabolism.isoprenoids.carotenoids	undefined	Y		plastid	

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AT1G06950	28	AT1G06950.1	ATTIC110/TIC110 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 110)	1016	ENV	Ch/E/IM	5.72	112.12	97.456592497391 5	0.0	2.5434075026084 9	982.0	protein targeting Tic	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope-inner-integral	2.0
AT1G07040	29	AT1G07040.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27030.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41035.1)	371			8.84	40.63	0.0	100.0	0.0	3.0		35.2 not assigned.unknown	chloroplast	Y	C	-	
AT1G07140	30	AT1G07140.1	SIRANBP (Ran-binding protein 1a); Ran GTPase binding	228			4.9	25.6	0.0	100.0	0.0	4.0		27.4 RNA.RNA binding	other (e.g. cytoplasm)			-	
AT1G07320	31	AT1G07320.3	RPL4 (ribosomal protein L4); poly(U) binding / structural constituent of ribosome	282	STR	Ch & other	8.92	30.55	14.667974840766 3	85.332025159233 7	0.0	128.0	translation stroma	29.2.1.1.1.2.4 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L4	chloroplast	Y	C	plastid ribosome	

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AT1G07640	32	AT1G07640.1	OBP2 (OBF BINDING PROTEIN 2); DNA binding / transcription factor	275			9.53	29.53	0.0	100.0	0.0	2.0		27.3.8 RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	undefined			-	
AT1G07660	33	AT1G07660.1	histone H4	103	THY-STR	other	11.47	11.41	14.832182545670 7	18.55641195487	66.611405499459 3	31.0	DNA binding	28.1.3 DNA.synthesis/chromatin structure.histone	undefined			nucleus	
AT1G07780	34	AT1G07780.1	PAI1 (PHOSPHORIBOSYLANTHRANILATE ISOMERASE 1); phosphoribosylanthranilate isomerase	275			8.63	29.63	0.0	100.0	0.0	7.0		13.1.6.5.3 amino acid metabolism.synthesis.aromatic aa.tryptophan.phosphoribosyanthranilate isomerase	chloroplast	Y	C	plastid stroma	
AT1G07920	35	AT1G07920.1	elongation factor 1-alpha / EF-1-alpha	449	THY	Ch/E & other	9.19	49.5	11.438783549487 9	9.302124380524 7 3	79.259092069987 4	68.0	translation cytosol	29.2.4 protein.synthesis.elongation	other (e.g. cytoplasm)			mitochondria	
AT1G08110	36	AT1G08110.1	lactoylglutathione lyase, putative / glyoxalase I, putative	185			5.14	20.84	0.0	100.0	0.0	4.0		13.2.3.2 amino acid metabolism.degradation.aspartate family.threonine	chloroplast			not plastid	
AT1G08380	37	AT1G08380.1	PSAO (photosystem I subunit O)	140			9.77	15.14	0.0	0.0	100.0	7.0		1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-integral	2.0

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AT1G08490	38	AT1G08490.1	ATCPNIFS/ATNFS2/ATSUFS/CPNIFS/SUFS (CHLOROPLASTIC NIFS-LIKE CYSTEINE DESULFURASE); cysteine desulfurase/ selenocysteine lyase/ transaminase	463			6.22	50.48	0.0	100.0	0.0	3.0		14 S-assimilation	chloroplast	Y	C	plastid stroma	
AT1G08520	39	AT1G08520.1	CHLD/PDE166 (PIGMENT DEFECTIVE 166); magnesium chelatase/ nucleoside-triphosphatase/ nucleotide binding	760	THY-STR		5.26	83.28	0.0	16.883402410516	83.116597589484	15.0		19.10 tetrapyrrole synthesis.magnesium chelatase	chloroplast	Y	C	plastid	

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AT1G08530	40	AT1G08530.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G09995.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G09995.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO70794.1)	257	ENV	Ch/E/IM	7.72	27.01	100.0	0.0	0.0	16.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	1.0
AT1G08550	41	AT1G08550.1	NPQ1 (NON-PHOTOCHEMICAL QUENCHING 1)	462	THY	Lum	5.18	52.01	0.0	0.0	100.0	16.0		16.1.4.21 secondary metabolism.isoprenoids.carotenoids. violaxanthin de-epoxidase	undefined			thylakoid-peripheral-lumenal-side	1.0
AT1G08640	42	AT1G08640.1	heat shock protein binding	294	ENV	Ch/E/IM	9.82	32.9	98.310536575869 6	0.0	1.6894634241304 2	59.0	chaperone and protease	26.29* misc.DnaJ domain with unknown function	chloroplast	Y	C	plastid	3.0
AT1G09130	43	AT1G09130.1	ATP-dependent Clp protease proteolytic subunit, putative	330	ENV-STR	Ch & other	8.63	36.3	51.591112627404 2	48.408887372595 8	0.0	141.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	2.0

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AT1G09200	44	AT1G09200.1	histone H3	136			11.29	15.26	0.0	39.394425184858 6	60.605574815141 4	4.0		28.1.3 DNA.synthesis/chromatin structure. histone	chloroplast	Y	C	nucleus	
AT1G09310	45	AT1G09310.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G56580.1); similar to unknown [Populus trichocarpa] (GB:ABK94207.1); contains InterPro domain Protein of unknown function DUF538 (InterPro:IPR007493)	179			5.36	19.94	0.0	100.0	0.0	3.0		35.2 not assigned. unknown	other (e.g. cytoplasm)			-	
AT1G09340	46	AT1G09340.1	CRB; binding / catalytic/ coenzyme binding	378	Mix	Ch	8.18	42.62	16.530230027286 3	47.315218750947 5	36.154551221766 3	713.0	RNA Binding	27 RNA	undefined			plastid stroma	
AT1G09780	47	AT1G09780.1	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglycerom utase, putative	557			5.31	60.58	0.0	100.0	0.0	4.0		4.11 glycolysis .phosphoglycerate mutase	other (e.g. cytoplasm)			cytosol	

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AT1G09795	48	AT1G09795.1	ATATP-PRT2 (ATP PHOSPHORIBOSYL TRANSFERASE 2); ATP phosphoribosyltransferase	413	STR		6.34	44.75	0.0	100.0	0.0	34.0		13.1.7.1 amino acid metabolism.synthesis.histidine.ATP phosphoribosyl transferase	chloroplast	Y	C	plastid stroma	
AT1G09830	49	AT1G09830.1	phosphoribosylamine--glycine ligase (PUR2)	532	STR		5.5	56.47	0.0	100.0	0.0	15.0		23.1.2.2 nucleotide metabolism.synthesis.purine.GAR Synthetase	chloroplast	Y	C	plastid stroma	
AT1G10510	50	AT1G10510.1	EMB2004 (EMBRYO DEFECTIVE 2004); protein binding	605	ENV	Ch/E & PG	7.18	64.72	100.0	0.0	0.0	150.0	RNA metabolism?	33.99 development.unspecified	chloroplast	Y	C	-	1.0
AT1G10630	51	AT1G10630.1	ATARFA1F; GTP binding / phospholipase activator/ protein binding	181	ENV	Ch/E ?	6.42	20.62	100.0	0.0	0.0	9.0	vesicular trafficking ?	29.3.4.99 protein.targeting.secretory pathway.unspecified	undefined		M	-	
AT1G10760	52	AT1G10760.1	SEX1 (STARCH EXCESS 1)	1399	STR	Ch/S & other	5.65	156.58	1.2830035960922 8	98.716996403907 7	0.0	297.0	metabolism carbon	2.2.2.3 major CHO metabolism.degradation.starch.glucan water dikinase	undefined		C	plastid stroma	

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AT1G11320	53	AT1G11320.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO60944.1)	424	ENV	Ch/E ?	6.54	46.89	100.0	0.0	0.0	2.0	unknown	35.2 not assigned. unknown	undefined			-	
AT1G11430	54	AT1G11430.1	plastid developmental protein DAG, putative	232			8.99	26.2	0.0	66.102150838928 1	33.897849161071 9	9.0		31.7* plastid differentiation	chloroplast	Y	C	plastid stroma	
AT1G11720	55	AT1G11720.1	ATSS3 (STARCH SYNTHASE 3); starch synthase/transferase, transferring glycosyl groups	1025			5.95	116.41	0.0	100.0	0.0	2.0		2.1.2.2 major CHO metabolism.synthesis.starch.starch synthase	chloroplast	Y	C	plastid stroma	
AT1G11750	56	AT1G11750.1	CLPP6 (Clp protease proteolytic subunit 6); endopeptidase Clp	271	STR-ENV	Ch/E & Ch/S	9.37	29.38	34.422571614963 9	65.577428385036 1	0.0	100.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT1G11860	57	AT1G11860.1	aminomethyltransferase, putative	408	THY-STR		8.55	44.44	0.0	24.528678553158 6	75.471321446841 4	13.0		13.2.5.2 amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	mitochondrion		M	-	
AT1G11870	58	AT1G11870.1	AtSRS (OVULE ABORTION 7); serine-tRNA ligase	512			6.49	57.18	0.0	100.0	0.0	9.0		29.1.11 protein.aa activation.serine-tRNA ligase	undefined	Y	M	mitochondria; plastid stroma	

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AT1G11930	59	AT1G11930.1	alanine racemase family protein	257			5.11	28.0	0.0	100.0	0.0	2.0		35.1 not assigned. no ontology	other (e.g. cytoplasm)			not plastid	
AT1G12230	60	AT1G12230.1	transaldolase, putative	405	ENV-STR	Ch/S	6.41	43.99	55.004980022510 5	34.408121182577 5	10.586898794912	25.0	metabolism carbon	7.2.2 OPP.non-reductive PP.transaldolase	chloroplast	Y	C	plastid stroma	
AT1G12250	61	AT1G12250.1	thylakoid lumenal protein-related	280	THY		8.72	30.06	0.0	0.0	100.0	23.0		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT1G12410	62	AT1G12410.1	CLPR2 (Clp protease proteolytic subunit 2); endopeptidase Clp	279	STR-ENV	Ch/E & Ch/S	9.19	31.2	41.004532408141 8	58.995467591858 2	0.0	100.0	chaperone and protease	29.5.5 protein.degradation.serine protease	undefined	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT1G12520	63	AT1G12520.1	CCS1 (copper chaperone for superoxide dismutase 1); superoxide dismutase copper chaperone	320	STR		4.93	27.19	0.0	100.0	0.0	10.0		15.2 metal handling. binding, chelation and storage	chloroplast	Y		plastid stroma	
AT1G12770	64	AT1G12770.1	EMB1586 (EMBRYO DEFECTIVE 1586)	551			9.29	60.71	0.0	100.0	0.0	3.0		27.5* RNA.DEAD/DEAH BOX helicase	undefined		M	-	

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AT1G12800	65	AT1G12800.1	S1 RNA-binding domain-containing protein	767			5.3	85.66	0.0	72.222630418809 7	27.777369581190 3	9.0		27.3.23 RNA.regulation of transcription.HSF, Heat-shock transcription factor family	chloroplast	Y	C	plastid stroma	
AT1G12840	66	AT1G12840.1	DET3 (DE-ETIOLATED 3)	375	ENV	other	5.4	42.62	100.0	0.0	0.0	18.0	transporter ATPase	34.1 transport.p- and v-ATPases	undefined		M	vacuole	
AT1G12900	67	AT1G12900.1	GAPA-2; glyceraldehyde-3-phosphate dehydrogenase	399	STR-ENV	Ch/S	8.15	42.84	18.321451248445 6	76.667405883243 3	5.011142868311 15	1976.0	metabolism carbon	1.3.4 PS.calvin cyle.GAP	chloroplast	Y	C	plastid stroma	
AT1G13270	68	AT1G13270.1	MAP1C (METHIONINE AMINOPEPTIDASE 1B); metalloexopeptidase	369			7.14	40.42	0.0	0.0	100.0	1.0		29.5.7 protein.degradation.metalloprotease	undefined	Y	C	mitochondria; plastid	
AT1G13280	69	AT1G13280.1	AOC4 (ALLENE OXIDE CYCLASE 4)	254			9.15	27.81				2.0		17.7.1.4 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase cyclase	chloroplast	Y	C	plastid stroma	
AT1G13440	70	AT1G13440.1	GAPC-2; glyceraldehyde-3-phosphate dehydrogenase	338	STR		6.67	36.91	0.0	100.0	0.0	23.0		4.9 glycolysis.glyceraldehyde 3-phosphate dehydrogenase	undefined			not plastid	

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AT1G13930	71	AT1G13930.1	similar to nodulin-related [Arabidopsis thaliana] (TAIR:AT2G03440.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63832.1)	155	STR-ENV	Ch & other	4.82	16.16	44.422901794894 4	55.577098205105 6	0.0	5.0	unknown	20.2.3 stress.abiotic.drought/salt	undefined			-	
AT1G14030	72	AT1G14030.1	ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, putative	482			5.01	54.61	0.0	100.0	0.0	8.0		1.3.13 PS.calvincyle.rubisco interacting	chloroplast	Y	C	plastid stroma	
AT1G14150	73	AT1G14150.1	oxygen evolving enhancer 3 (PsbQ) family protein	190			8.79	22.15	0.0	0.0	100.0	8.0		1.1.6 PS.lightreaction.NADH DH	undefined	Y	C	thylakoid-peripheral-lumenal-side	
AT1G14345	74	AT1G14345.1	oxidoreductase	196	THY	Ch/Th	9.81	21.22	9.4130208906913 6	0.0	90.586979109308 6	18.0	redox ?	35.2 not assigned.unknown	chloroplast	Y	C	thylakoid-integral	1.0
AT1G14410	75	AT1G14410.1	ATWHY1/PTAC1 (A. THALIANA WHIRLY 1); DNA binding / telomeric DNA binding	263			9.38	29.05	0.0	100.0	0.0	7.0		27.3.67 RNA.regulation of transcription.putative transcription regulator	undefined	Y	C	plastid stroma	1.0

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AT1G14810	76	AT1G14810.1	semialdehyde dehydrogenase family protein	375	STR		6.52	40.74	0.0	96.008062014685 3	3.9919379853146 7	102.0		13.1.3.6.1.2 amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate semialdehyde dehydrogenase	undefined	Y	C	plastid stroma	
AT1G15140	77	AT1G15140.1	oxidoreductase NAD-binding domain-containing protein	295	STR		7.79	31.92	0.0	100.0	0.0	95.0		26.7 misc.oxidases - copper, flavone etc.	chloroplast	Y	C	plastid stroma	
AT1G15390	78	AT1G15390.1	PDF1A (PEPTIDE DEFORMYLASE 1A); peptide deformylase	269			8.6	29.99	0.0	100.0	0.0	5.0		29.4 protein.postranslational modification	undefined	Y	C	plastid; mitochondria	
AT1G15500	79	AT1G15500.1	ATNTT2; ATP:ADP antiporter	618	ENV	Ch/E/IM	9.51	67.53	100.0	0.0	0.0	36.0	transporter ATP/ADP	34.8 transport.metabolite transporters at the envelope membrane	undefined	Y	M	envelope-inner-integral	11.0
AT1G15690	80	AT1G15690.1	AVP1 (vacuolar-type H+-pumping pyrophosphatase 1); ATPase	770	ENV	Ch/E & other	5.12	80.82	100.0	0.0	0.0	35.0	transporter ATPase	23.4.99 nucleotide metabolism.phosphotransfer and pyrophosphatases.misc	secreted		S	-	16.0

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AT1G15730	81	AT1G15730.1	PRLI-interacting factor L, putative	448	STR		5.25	50.25	0.0	100.0	0.0	27.0		31.1 cell.organisation	undefined	Y	C	plastid	
AT1G15820	82	AT1G15820.1	LHCB6 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding	258	THY	Ch	6.75	27.52	1.5360187025233 2	0.4804248418370 36	97.983556455639 6	631.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	undefined	Y	M	thylakoid-integral	2.0
AT1G15980	83	AT1G15980.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO49411.1); contains domain G3DSA:3.40.50.2000 (G3DSA:3.40.50.2000); contains domain SSF53756 (SSF53756)	461	THY		6.49	51.02	0.0	0.0	100.0	17.0		1.1.6 PS.lightreaction.NADH DH	chloroplast	Y	C	thylakoid	
AT1G16080	84	AT1G16080.1	similar to unknown [Populus trichocarpa] (GB:ABK94042.1)	313	STR		6.38	34.13	0.0	100.0	0.0	118.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	

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AT1G16720	85	AT1G16720.1	HCF173 (HIGH CHLOROPHYLL FLUORESCENCE PHENOTYPE 173); binding / catalytic/ oxidoreductase/ transcription repressor	598	STR		9.14	65.7	0.0	100.0	0.0	44.0		29.2.99 protein.synthesis.misc	chloroplast	Y	C	plastid	
AT1G16790	86	AT1G16790.1	ribosomal protein-related	144	ENV	Ch	9.55	15.45	100.0	0.0	0.0	19.0	unknown	29.2.1.99.99 protein.synthesis.ribosomal protein.unknown.unknown	undefined			-	
AT1G16880	87	AT1G16880.1	uridylyltransferase-related	290	STR-ENV	Ch	4.97	31.29	25.686152735534 1	74.313847264465 9	0.0	104.0	metabolism carbon	3.8.3 minor CHO metabolism.galactose.galactose-1-phosphate uridyl transferases	chloroplast	Y	C	plastid stroma; thylakoid-inner-peripheral-stromal-side	
AT1G17050	88	AT1G17050.1	SPS2 (SOLANESYL DIPHOSPHATE SYNTHASE 2); dimethylallyltransferase/ trans-octaprenyltransferase	417	STR		5.44	46.04	0.0	100.0	0.0	17.0		16.1.1 secondary metabolism.isoprenoids.non-mevalonate pathway	undefined	Y	C	plastid stroma	

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AT1G17160	89	AT1G17160.1	pfkB-type carbohydrate kinase family protein	379			6.11	40.19	0.0	100.0	0.0	3.0		3.5 minor CHO metabolism.others	chloroplast	Y	C	-	
AT1G17220	90	AT1G17220.1	FUG1 (FU-GAERI1); translation initiation factor	1026	STR		7.14	109.74	0.0	100.0	0.0	22.0		29.2.3 protein.synthesis.initiation	undefined	Y	C	plastid stroma	
AT1G17580	91	AT1G17580.1	MYA1 (ARABIDOPSIS MYOSIN); motor/ protein binding	1520	ENV-STR	Ch/E ?	8.56	172.91	76.174644552747 2	23.825355447252 8	0.0	5.0	plastid positioning ?	31.1 cell.organisation	undefined			-	
AT1G17650	92	AT1G17650.1	phosphogluconate dehydrogenase (decarboxylating)	358	STR		8.68	37.78	0.0	100.0	0.0	52.0		7.1.3 OPP.oxidative PP.6-phosphogluconate dehydrogenase	chloroplast	Y	C	plastid stroma	
AT1G17745	93	AT1G17745.1	PGDH (3-PHOSPHOGLYCERATE DEHYDROGENASE); phosphoglycerate dehydrogenase	624	STR	Ch/S	5.8	66.45	6.0101069315745 2	93.989893068425 5	0.0	70.0	metabolism aa Ser	13.1.5.1.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	chloroplast	Y	C	plastid stroma	
AT1G18060	94	AT1G18060.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO68142.1)	226			9.67	25.19				4.0		35.2 not assigned.unknown	undefined	Y	C	thylakoid	

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AT1G18170	95	AT1G18170.1	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	247			8.96	26.53	0.0	0.0	100.0	9.0		29.6 protein.folding	undefined	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT1G18360	96	AT1G18360.1	hydrolase, alpha/beta fold family protein	382	ENV	Ch/E/IM	9.61	41.96	100.0	0.0	0.0	7.0	metabolism lipid	35.1 not assigned. no ontology	chloroplast	Y	C	-	
AT1G18500	97	AT1G18500.1	IPMS1/MAML-4 (METHYLTHIOALKYLMALATE SYNTHASE-LIKE 4); 2-isopropylmalate synthase	631	STR		6.15	68.67	0.0	100.0	0.0	39.0		13.1.4.4.1 amino acid metabolism.synthesis.branched chain group.leucine specific.2-isopropylmalate synthase	chloroplast	Y	C	plastid stroma	
AT1G18640	98	AT1G18640.1	PSP (3-PHOSPHOSERINE PHOSPHATASE)	295			6.04	32.31	0.0	100.0	0.0	6.0		13.1.5.1.3 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoserine phosphatase	undefined		C	plastid	
AT1G19740	99	AT1G19740.1	ATP-dependent protease La (LON) domain-containing protein	278	STR		8.29	31.37	0.0	100.0	0.0	10.0		29.5.5 protein.degradation.serine protease	chloroplast	Y	C	-	

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AT1G19800	100	AT1G19800.1	TGD1 (TRIGALACTOSYLDIACYLGLYCEROL 1)	350	ENV	Ch/E/IM	9.0	37.9	100.0	0.0	0.0	20.0	transporter lipids	11.15* lipid metabolism.transport	undefined			envelope-inner-integral	5.0
AT1G19910	101	AT1G19910.1	AVA-P2 (vacuolar-H+-pumping ATPase 16 kDa proteolipid subunit 2); ATPase	165	ENV	other	8.61	16.64	100.0	0.0	0.0	6.0	transporter ATPase	34.1.1 transport.p- and v-ATPases.H+-transporting two-sector ATPase	secreted	Y	S	-	3.0
AT1G19920	102	AT1G19920.1	APS2 (ATP SULFURYLASE PRECURSOR)	476	STR		6.14	53.63	0.0	100.0	0.0	42.0		14.1 S-assimilation.APS	chloroplast	Y	C	-	
AT1G20010	103	AT1G20010.1	TUB5 (tubulin beta-5 chain)	449	STR		4.66	50.34	0.0	100.0	0.0	21.0		31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT1G20020	104	AT1G20020.1	ATLFNR2 (LEAF FNR 2); NADPH dehydrogenase/ oxidoreductase/ poly(U) binding	369	STR-THY	Ch	8.5	41.16	10.739206640119 9	56.877907251912 1	32.38288 6107968	498.0	redox	1.1.7 PS.lightreaction.ferredoxin reductase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT1G20340	105	AT1G20340.1	DRT112 (DNA-damage-repair/toleration protein 112); copper ion binding / electron carrier	167	THY	Ch/Th/Lum	5.06	16.98	11.126442635028 8	13.920193639208 4	74.953363725762 8	15.0	PS b6/f PSI electron transfer	1.1.5.1 PS.lightreaction.other electron carrier (ox/red).plastocyanin	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT1G20440	106	AT1G20440.1	COR47 (cold regulated 47)	265			4.75	29.89	0.0	100.0	0.0	7.0		20.2.99 stress.abiotic.unspecified	other (e.g. cytoplasm)			-	

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AT1G20450	107	AT1G20450.1	ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDRATION 10)	260			5.11	29.54	0.0	100.0	0.0	4.0		20.2.99 stress.abiotic.unspecified	other (e.g. cytoplasm)			-	
AT1G20620	108	AT1G20620.1	CAT3 (CATALASE 3); catalase	492	STR	Ch/E ?	7.31	56.69	7.9386294569194 8	84.421565329414 5	7.6398052136659 8	188.0	stress oxidative	21.6 redox.dismutases and catalases	undefined			peroxisome	
AT1G20816	109	AT1G20816.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76405.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO66270.1)	167	ENV	Ch/E/OM	9.51	19.78	100.0	0.0	0.0	5.0	transporter ion channel	35.2 not assigned. unknown	undefined			-	
AT1G20830	110	AT1G20830.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO66272.1)	349	ENV	Ch/E/IM	9.09	39.41	100.0	0.0	0.0	11.0	unknown	31.2.5 cell.division.plastid; 35.2 not assigned. unknown	chloroplast	Y	C	envelope-inner	1.0
AT1G21200	111	AT1G21200.1	transcription factor	443			5.88	50.93	0.0	100.0	0.0	2.0		27.3.30 RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family	undefined			-	
AT1G21440	112	AT1G21440.1	mutase family protein	336	STR		6.67	36.3	0.0	100.0	0.0	20.0		35.2 not assigned. unknown	undefined	Y	C	plastid stroma	

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AT1G21500	113	AT1G21500.1	similar to hypothetical protein OsI_030994 [Oryza sativa (indica cultivar-group)] (GB:EAZ09762.1); similar to Os09g0517000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063677.1); similar to unknown protein [Oryza sativa (japonica cultivar-group	126	THY	Ch/E ?	10.65	13.25	6.0984045935792 9	0.0	93.901595406420 7	26.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	
AT1G21650	114	AT1G21650.1	ATP binding	1579	ENV	Ch/E ?	5.39	177.64	100.0	0.0	0.0	15.0	protein targeting ?	29.3.3 protein.targeting.chloroplast	chloroplast			-	
AT1G22700	115	AT1G22700.1	tetratricopeptide repeat (TPR)-containing protein	301			9.41	33.66	0.0	0.0	100.0	8.0		29.8 protein assembly and cofactor ligation	undefined		C	thylakoid-integral	1.0
AT1G22740	116	AT1G22740.1	RAB7 (Ras-related protein 7); GTP binding	203	ENV	Ch/E ?	5.28	22.94	100.0	0.0	0.0	4.0	signalling / SNARE effector	30.5 signalling.G-proteins	undefined		M	-	

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AT1G22780	117	AT1G22780.1	PFL (POINTED FIRST LEAVES); structural constituent of ribosome	152	ENV	Ch/E & other	10.53	17.54	100.0	0.0	0.0	4.0	translation cytosol	29.2.1.2.1.18 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S18	undefined			cytosol	
AT1G22940	118	AT1G22940.1	TH1 (THIAMINE REQUIRING 1); catalytic/ phosphomethylpyrimidine kinase/ thiamin-phosphate diphosphorylase	522	STR		6.1	55.81	0.0	100.0	0.0	10.0		18.2.2 Co-factor and vitamine metabolism.thiamine.hydroxymethyl pyrimidine kinase	undefined	Y	M	-	
AT1G23180	119	AT1G23180.1	armadillo /beta-catenin repeat family protein	834	STR		5.33	91.69	0.0	100.0	0.0	45.0		35.1.3 not assigned.no ontology.armadillo /beta-catenin repeat family protein	undefined		C	plastid	
AT1G23190	120	AT1G23190.1	phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	583			5.91	63.17	0.0	100.0	0.0	7.0		4.2 glycolysis.PGM	other (e.g. cytoplasm)	Y		-	

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AT1G23310	121	AT1G23310.1	GGT1 (ALANINE-2-OXOGLUTARATE AMINOTRANSFERASE 1)	481	STR		6.49	53.3	0.0	100.0	0.0	12.0		1.2.3 PS.aminotransferases peroxisomal	other (e.g. cytoplasm)			peroxisome	
AT1G23730	122	AT1G23730.1	carbonic anhydrase, putative / carbonate dehydratase, putative	258	ENV-STR	other	6.53	28.82	61.517808107723 3	38.482191892276 7	0.0	3.0	metabolism carbon	8.3 TCA / org.transformation.carbonic anhydrases	other (e.g. cytoplasm)			cytosol	
AT1G23740	123	AT1G23740.1	oxidoreductase, zinc-binding dehydrogenase family protein	386	STR		8.46	40.98	0.0	100.0	0.0	162.0		26.7 misc.oxidases - copper, flavone etc.	undefined	Y	C	plastid stroma	
AT1G24040	124	AT1G24040.1	GCN5-related N-acetyltransferase (GNAT) family protein	319	ENV	Ch/E ?	6.47	36.02	100.0	0.0	0.0	2.0	unknown	26.24 misc.GCN5-related N-acetyltransferase	chloroplast	Y	C	-	
AT1G24360	125	AT1G24360.1	3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase	319	STR	Ch/E/IM	9.45	33.54	10.724391344857 8	73.794549609410 2	15.481059045732	66.0	metabolism lipid	11.1.4 lipid metabolism.FA synthesis and FA elongation.ACP oxoacyl reductase	undefined	Y	C	plastid stroma	
AT1G25290	126	AT1G25290.1	rhomboid family protein	343	ENV	Ch/E/IM	10.79	38.22	100.0	0.0	0.0	4.0	chaperone and protease	29.5.5 protein.degradation.serine protease	undefined		C	golgi	3.0

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AT1G25375	127	AT1G25375.1	metallo-beta-lactamase family protein	524	ENV	Ch/E	6.52	58.06	100.0	0.0	0.0	6.0	hydrolase ?	35.1 not assigned.no ontology	other (e.g. cytoplasm)			-	1.0
AT1G26230	128	AT1G26230.1	chaperonin, putative	611	STR-ENV	Ch/E ?	9.22	66.79	20.368010155719 9	79.631989844280 1	0.0	40.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid	
AT1G26340	129	AT1G26340.1	B5 #6 (cytochrome b5 family protein #6); heme binding / transition metal ion binding	135	ENV	Ch/E & other	4.49	15.22	100.0	0.0	0.0	3.0	metabolism lipid	21.3 redox.heme	other (e.g. cytoplasm)			envelope	1.0
AT1G26630	130	AT1G26630.1	FBR12 (FUMONISIN B1-RESISTANT12); translation initiation factor	159			5.54	17.14	0.0	0.0	100.0	2.0		29.2.3 protein.synthesis.initiation	other (e.g. cytoplasm)			-	
AT1G27400	131	AT1G27400.1	60S ribosomal protein L17 (RPL17A)	176	ENV	Ch/E & other	10.11	19.89	100.0	0.0	0.0	3.0	translation cytosol	29.2.1.2.2.17 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L17	other (e.g. cytoplasm)			cytosol	
AT1G27450	132	AT1G27450.1	APT1; adenine phosphoribosyltransferase	243	STR		8.65	26.39	0.0	100.0	0.0	19.0		23.3.1.1 nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	chloroplast	Y	C	cytosol	
AT1G27900	133	AT1G27900.1	RNA helicase, putative	700			8.19	78.37	0.0	24.528678553158 6	75.471321446841 4	2.0		27.1.2 RNA.processing.RNA helicase	undefined			-	

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AT1G28140	134	AT1G28140.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO68697.1)	280			8.51	30.27	0.0	0.0	100.0	4.0		9.7 mitochondrial electron transport / ATP synthesis.cytochrome c oxidase	undefined	Y	M	plastid	6.0
AT1G28530	135	AT1G28530.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO66376.1)	614	ENV	Ch/E/IM	7.99	68.45	100.0	0.0	0.0	2.0	transporter ABC ?	35.2 not assigned. unknown	chloroplast	Y	C	-	1.0
AT1G29670	136	AT1G29670.1	GDSL-motif lipase/hydrolase family protein	363	THY		8.84	39.87	0.0	0.0	100.0	14.0		26.28 misc.GDSL-motif lipase	secreted		S	-	
AT1G29700	137	AT1G29700.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO42101.1); contains domain SSF56281 (SSF56281)	350	ENV-STR	Ch/E/IM	5.83	38.15	76.174644552747 2	23.825355447252 8	0.0	4.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	plastid	
AT1G29840	138	AT1G29840.1	esterase/lipase/thioesterase family protein	263			5.87	29.56	0.0	100.0	0.0	1.0		35.1 not assigned. no ontology	undefined			-	

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AT1G29900	139	AT1G29900.1	CARB (CARBAMOYL PHOSPHATE SYNTHETASE B); ATP binding / carbamoyl-phosphate synthase	1187	STR		5.53	129.95	0.0	100.0	0.0	101.0		23.1.1.1 nucleotide metabolism.synthesis.pyrimidine.carbamoyl phosphate synthetase	chloroplast	Y	C	plastid stroma	
AT1G29910	140	AT1G29910.1	CAB3 (CHLOROPHYLL A/B BINDING PROTEIN 3); chlorophyll binding	267	THY	Ch/Th & other	5.28	28.22	1.3289221372827 6	0.6754323438084 48	97.995645518908 8	1047.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0
AT1G29930	141	AT1G29930.1	CAB1 (CHLOROPHYLL A/B BINDING PROTEIN 1); chlorophyll binding	267	THY	Ch/Th	5.46	28.24	1.3289221372827 6	0.6754323438084 48	97.995645518908 8	1049.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0
AT1G30120	142	AT1G30120.1	PDH-E1 BETA (PYRUVATE DEHYDROGENASE E1 BETA); pyruvate dehydrogenase (acetyl-transferring)	406	ENV-STR	Ch/E/IM	5.91	44.24	51.591112627404 2	48.408887372595 8	0.0	30.0	metabolism lipid	11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	chloroplast	Y	C	-	

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AT1G30380	143	AT1G30380.1	PSAK (PHOTOSYSTEM I SUBUNIT K)	130	THY		10.51	13.2	0.0	0.0	100.0	148.0		1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	undefined	Y	C	thylakoid-integral	2.0
AT1G30410	144	AT1G30410.1	ATMRP13 (Arabidopsis thaliana multidrug resistance-associated protein 13)	1495			8.4	167.95	0.0	100.0	0.0	5.0		34.16 transport.ABC transporters and multidrug resistance systems	other (e.g. cytoplasm)			-	13.0
AT1G30510	145	AT1G30510.3	ATRFNR2 (ROOT FNR 2); oxidoreductase	381			8.77	42.66	0.0	100.0	0.0	7.0		7.3 OPP.electron transfer	chloroplast	Y	C	-	
AT1G31160	146	AT1G31160.1	zinc-binding protein, putative / protein kinase C inhibitor, putative	187			9.22	20.4	0.0	100.0	0.0	4.0		29.4.2* protein.postranslational modification.kinase inhibitor	undefined	Y	C	-	
AT1G31180	147	AT1G31180.1	3-isopropylmalate dehydrogenase, chloroplast, putative	404	STR		5.6	43.84	0.0	100.0	0.0	86.0		13.1.4.4.3 amino acid metabolism.synthesis.branched chain group.leucine specific.3-isopropylmalate dehydrogenase	undefined		M	plastid stroma	

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AT1G31190	148	AT1G31190.1	inositol monophosphatase family protein	371	STR		6.76	40.44	0.0	100.0	0.0	40.0		3.4.5 minor CHO metabolism.myo-inositol.inositol phosphatase	chloroplast	Y	C	plastid stroma	
AT1G31220	149	AT1G31220.1	phosphoribosylglycinamide formyltransferase	292			8.92	32.17	0.0	100.0	0.0	3.0		23.1.2.3 nucleotide metabolism.synthesis.purine.GAR transformylase	chloroplast	Y	C	-	
AT1G31230	150	AT1G31230.1	AK-HSDH/AK-HSDH I (ASPARTATE KINASE-HOMOSERINE DEHYDROGENASE I); aspartate kinase/homoserine dehydrogenase	911	STR		6.33	99.4	0.0	100.0	0.0	119.0		13.1.3.6.1.1 amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate kinase	undefined	Y	C	plastid stroma	
AT1G31330	151	AT1G31330.1	PSAF (photosystem I subunit F)	221	THY-ENV	Ch	9.57	24.17	18.777548853243 2	0.177972914614924	81.044478232141 8	316.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-integral	2.0
AT1G31410	152	AT1G31410.1	putrescine-binding periplasmic protein-related	524	ENV	Ch/E/IM	9.2	58.29	100.0	0.0	0.0	23.0	transporter solute binding ?	35.1 not assigned.no ontology	chloroplast		C	-	

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AT1G31800	153	AT1G31800.1	CYP97A3/LUT5 (CYTOCHROME P450-TYPE MONOOXYGENASE 97A3); carotene beta-ring hydroxylase/ oxygen binding	595	ENV	Ch/E/IM	5.81	66.84	100.0	0.0	0.0	37.0	cytochrome P450	26.10 misc.cytochrome P450	chloroplast	Y	C	plastid	
AT1G31860	154	AT1G31860.1	AT-IE (Arabidopsis thaliana bifunctional HisI-HisE protein)	281	STR		5.89	31.66	0.0	100.0	0.0	29.0		13.1.7.2 amino acid metabolism.synthesis.histidine.phosphoribosyl-ATP diphosphatase	undefined	Y	M	plastid stroma	
AT1G32060	155	AT1G32060.1	PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/ protein binding	395	STR	Ch	5.7	44.46	14.223558668872 3	83.670570804366 4	2.1058705267612 5	794.0	metabolism carbon	1.3.12 PS.calvin cyle.PRK	chloroplast	Y	C	plastid stroma	
AT1G32080	156	AT1G32080.1	membrane protein, putative	512	ENV	Ch/E/IM	9.63	54.01	98.82585344238	0.0	1.1741465576200 1	165.0	transporter ?	34.8 transport. metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	12.0

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AT1G32160	157	AT1G32160.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17800.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17800.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO63331.1); contains InterPro domain Protein of unkno	406	STR		5.53	45.86	0.0	100.0	0.0	17.0		35.2 not assigned. unknown	chloroplast	Y	C	-	
AT1G32200	158	AT1G32200.1	ATS1 (ACYLTRANSFERASE 1)	459	STR		6.11	50.42	0.0	100.0	0.0	55.0		11.3.1 lipid metabolism.Phospholipid synthesis.1-acylglycerol-3-phosphate O-acyltransferase	undefined	Y	C	plastid stroma	
AT1G32220	159	AT1G32220.1	binding / catalytic/ coenzyme binding	296			5.56	31.97	0.0	100.0	0.0	9.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma; plastoglobules	

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AT1G32500	160	AT1G32500.1	ATNAP6 (NON-INTRINSIC ABC PROTEIN 6); protein binding	475	STR		5.66	52.82	0.0	100.0	0.0	29.0		14 S-assimilation	chloroplast	Y	C	plastid stroma	
AT1G32550	161	AT1G32550.1	ferredoxin family protein	181	ENV-STR	CH/E/IM	5.57	20.37	61.517808107723 3	38.482191892276 7	0.0	6.0	redox	26.30 misc.other Ferredoxins and Rieske domain	undefined	Y	C	-	
AT1G32900	162	AT1G32900.1	starch synthase, putative	610			8.76	66.88	0.0	0.0	100.0	4.0		2.1.2.2 major CHO metabolism.synthesis.starch.starch synthase	chloroplast	Y	C	plastid stroma	
AT1G32990	163	AT1G32990.1	PRPL11 (PLASTID RIBOSOMAL PROTEIN L11); structural constituent of ribosome	222	Mix	Ch/S	9.68	23.14	25.233469141679 6	46.746950707629 9	28.019580150690 5	148.0	translation stroma	29.2.1.1.1.2.11 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L11	chloroplast	Y	C	plastid ribosome	

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AT1G33780	164	AT1G33780.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G29240.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G29240.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64828.1); contains InterPro domain Protein of unknown	325			6.62	36.39	0.0	100.0	0.0	5.0		35.1 not assigned. no ontology	chloroplast	Y	C	-	
AT1G33810	165	AT1G33810.1	similar to unknown [Populus trichocarpa] (GB:ABK94119.1)	138	ENV	Ch/E ?	8.82	15.69	89.553617154618 2	0.0	10.446382845381 8	39.0	metabolism lipid ?	35.2 not assigned. unknown	other (e.g. cytoplasm)			thylakoid	
AT1G34000	166	AT1G34000.1	OHP2 (ONE-HELIX PROTEIN 2)	172	THY	Ch/Th	9.43	18.66	5.1854294154885	0.0	94.814570584511 5	34.0	PS PSII stress oxidative	1.1.8* light stress chlorophyll binding	chloroplast	Y	C	thylakoid-integral	

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AT1G34430	167	AT1G34430.1	EMB3003 (EMBRYO DEFECTIVE 3003); dihydrolipoyllysine-residue acetyltransferase	465	Mix	Ch/E/IM	8.8	48.3	47.665093752852 7	18.974255933473	33.360650313674 3	46.0	metabolism lipid	11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	undefined	Y	C	envelope-inner-peripheral-stromal-side	
AT1G35340	168	AT1G35340.1	ATP-dependent protease La (LON) domain-containing protein	316			8.54	32.82	0.0	100.0	0.0	5.0		29.5 protein.degradation	chloroplast	Y	C	-	
AT1G35420	169	AT1G35420.1	dienelactone hydrolase family protein	310			5.27	34.16	0.0	100.0	0.0	6.0		35.2 not assigned.unknown	chloroplast	Y	C	plastid stroma	
AT1G35680	170	AT1G35680.1	50S ribosomal protein L21, chloroplast / CL21 (RPL21)	220	STR-ENV	Ch/S & other	9.31	24.03	31.353766567662 4	68.646233432337 6	0.0	48.0	translation stroma	29.2.1.1.1.2.21 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L21	chloroplast	Y	C	plastid ribosome	
AT1G35720	171	AT1G35720.1	ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding	317			5.21	36.2	0.0	100.0	0.0	3.0		31.1 cell.organisation	other (e.g. cytoplasm)			plastid	

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AT1G35730	172	AT1G35730.1	APUM9 (ARABIDOPSIS PUMILIO 9); RNA binding	564			8.29	63.25	0.0	100.0	0.0	1.0		35.1.12 not assigned. no ontology. pumilio/Puf RNA-binding domain-containing protein	other (e.g. cytoplasm)			-	
AT1G36280	173	AT1G36280.1	adenylosuccinate lyase, putative / adenylosuccinase, putative	527	STR		7.0	58.81	0.0	100.0	0.0	74.0		23.1.2.8 nucleotide metabolism.synthesis.purine.SAICAR lyase	chloroplast	Y	C	plastid stroma	
AT1G36390	174	AT1G36390.1	co-chaperone grpE family protein	279	STR		9.43	31.22	0.0	100.0	0.0	18.0		29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT1G42960	175	AT1G42960.1	expressed protein localized to the inner membrane of the chloroplast.	168	ENV	Ch/E & Ch/Th	8.54	17.82	91.416986599674 5	0.0	8.5830134003255 1	49.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	1.0
AT1G42970	176	AT1G42970.1	GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase	447	STR-ENV	Ch	6.33	47.66	16.787019346807 2	78.216549978924 7	4.9964306742681	2212.0	metabolism carbon	1.3.4 PS.calvin cyle.GAP	undefined	Y	C	plastid stroma	

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AT1G43560	177	AT1G43560.1	ATY2 (Arabidopsis thioredoxin y2); thiol-disulfide exchange intermediate	167	STR		8.44	18.59	0.0	100.0	0.0	16.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	
AT1G43670	178	AT1G43670.1	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	341			5.27	37.28	0.0	100.0	0.0	3.0		2.1.1.3 major CHO metabolism.synthesis.sucrose.FBPase	other (e.g. cytoplasm)			-	
AT1G44318	179	AT1G44318.1	HEMB2; porphobilinogen synthase	406			8.38	44.87	0.0	100.0	0.0	6.0		19.4 tetrapyrrole synthesis.ALA dehydratase	undefined	Y		-	
AT1G44575	180	AT1G44575.1	NPQ4 (NONPHOTOCHEMICAL QUENCHING)	265	THY	Ch/Th	9.24	28.0	0.98926397733534 3	0.0	99.010736022664 7	384.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined	Y	C	thylakoid-integral	4.0
AT1G44920	181	AT1G44920.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO61509.1)	258	ENV	Ch/E/IM	10.03	27.71	100.0	0.0	0.0	4.0	unknown	35.2 not assigned. unknown	undefined	Y	C	-	4.0

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AT1G45474	182	AT1G45474.1	LHCA5 (Photosystem I light harvesting complex gene 5)	256			6.65	27.8	0.0	0.0	100.0	4.0		1.1.2.1 PS.lightreaction.photosystem I.LHC-I	undefined		M	thylakoid-integral	
AT1G47900	183	AT1G47900.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G19835.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48232.1); similar to hypothetical protein OsI_010472 [Oryza sativa (indica cultivar-group)] (GB:EAY89239.1); similar to h	1054			4.89	118.54	0.0	100.0	0.0	2.0		35.2 not assigned. unknown	undefined			-	
AT1G48030	184	AT1G48030.1	dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1)	507			6.95	53.98	0.0	100.0	0.0	8.0		8.1.1.3 TCA / org.transformation. TCA.pyruvate DH.E3	mitochondrion	Y	M	mitochondria	

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AT1G48350	185	AT1G48350.1	ribosomal protein L18 family protein	170	STR	Ch/S	9.92	18.72	15.064952499222 1	80.102420606687 3	4.832626894090 62	64.0	translation stroma	29.2.1.1.1.2.18 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L18	chloroplast	Y	C	plastid ribosome	
AT1G48420	186	AT1G48420.1	D-CDES (D-CYSTEINE DESULFHYDRASE); 1-aminocyclopropane-1-carboxylate deaminase/ D-cysteine desulfhydrase/ catalytic	401	STR		6.87	43.9	0.0	100.0	0.0	12.0		17.5.1 hormone metabolism.ethylene.synthesis-degradation	undefined		M	plastid	

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AT1G48460	187	AT1G48460.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63040.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63040.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61244.1)	340	ENV	Ch/E/IM	9.68	38.07	100.0	0.0	0.0	24.0	transporter ion channel ?	35.2 not assigned. unknown	chloroplast	Y	C	-	5.0
AT1G48520	188	AT1G48520.1	GATB (GLU-ADT SUBUNIT B); glutaminyl-tRNA synthase (glutamine-hydrolyzing)	550	STR		7.51	60.94	0.0	100.0	0.0	55.0		29.1.50* protein.aa activation.glutamate-tRNA amidotransferase	mitochondrion	Y	M	mitochondria; plastid stroma	
AT1G48850	189	AT1G48850.1	EMB1144 (EMBRYO DEFECTIVE 1144); chorismate synthase	436	STR		8.36	47.31	0.0	100.0	0.0	20.0		13.1.6.1.7 amino acid metabolism.synthesis.aromatic aa.chorismate.chorismate synthase	chloroplast	Y	C	plastid	

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AT1G49240	190	AT1G49240.1	ACT8 (ACTIN 8); structural constituent of cytoskeleton	377	STR-ENV	Ch/E & other	5.36	41.86	27.333093838892 5	72.666906161107 5	0.0	20.0	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT1G49510	191	AT1G49510.1	EMB1273 (EMBRYO DEFECTIVE 1273)	240	ENV	Ch/E/IM	9.73	27.38	100.0	0.0	0.0	5.0	unknown	33.99 development.unspecified	undefined	Y	C	-	4.0
AT1G49650	192	AT1G49650.1	cell death associated protein-related	374			6.5	41.69	0.0	100.0	0.0	2.0		35.1 not assigned. no ontology	undefined	Y	M	-	
AT1G49970	193	AT1G49970.1	CLPR1 (Clp protease proteolytic subunit 5); endopeptidase Clp	387	STR-ENV	Ch/E & Ch/S	8.81	42.62	37.774764448955 6	62.225235551044 3	0.0	109.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-inner-peripheral-stromal-side	
AT1G50250	194	AT1G50250.1	FTSH1 (FtsH protease 1); ATP-dependent peptidase/ ATPase/ metallopeptidase	716	THY-ENV	Ch/E & Ch/Th/Lum	5.63	76.76	18.211602535796 7	0.0	81.788397464203 3	276.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	thylakoid-integral	2.0
AT1G50320	195	AT1G50320.1	ATHX (THIOREDOXIN X); thiol-disulfide exchange intermediate	182			9.06	19.64	0.0	100.0	0.0	2.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	
AT1G50450	196	AT1G50450.1	binding / catalytic	428	THY	Ch/E ?	8.18	46.56	11.096761222293 1	3.4707648717855 4	85.432473905921 3	10.0	unknown	35.2 not assigned. unknown	undefined		M	plastid	

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AT1G50730	197	AT1G50730.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO38919.1); contains domain PTHR13673 (PTHR13673)	1013			5.23	113.89	0.0	100.0	0.0	2.0		35.2 not assigned. unknown	undefined		M	-	2.0
AT1G51060	198	AT1G51060.1	HTA10; DNA binding	132	THY-ENV	other	10.09	13.93	19.371564701817 6	6.0588981714338	74.569537126748 6	9.0	DNA binding	28.1.3 DNA.synthesis/chromatin structure. histone	undefined	Y	M	-	
AT1G51100	199	AT1G51100.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO39038.1)	211	STR		9.36	24.16	0.0	100.0	0.0	16.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT1G51110	200	AT1G51110.1	plastid-lipid associated protein PAP / fibrillin family protein	409	THY-ENV	Ch	8.1	45.76	46.407376457091 1	0.0	53.592623542908 9	36.0	PAP_fibrillin	26.31* misc.fibrillins	chloroplast	Y	C	thylakoid-peripheral-stromal-side	

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AT1G51900	201	AT1G51900.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G14830.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24094.1); contains InterPro domain Protein of unknown function DUF292, eukaryotic (InterPro:IPR005061)	774			5.25	92.19	0.0	100.0	0.0	2.0		35.2 not assigned. unknown	mitochondrion	Y	M	-	
AT1G51965	202	AT1G51965.1	pentatricopeptide (PPR) repeat-containing protein	650			8.65	73.88	0.0	100.0	0.0	3.0		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	undefined	Y	M	-	

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AT1G52220	203	AT1G52220.1	similar to PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA) [Arabidopsis thaliana] (TAIR:AT2G46820.2); similar to PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA), DNA binding [Arabidopsis thaliana] (TAIR:AT2G4	156			9.0	16.94	0.0	0.0	100.0	8.0		1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid	2.0
AT1G52230	204	AT1G52230.1	PSAH-2/PSAH2/PSI-H (PHOTOSYSTEM I SUBUNIT H-2)	145	THY	Ch/Th	9.89	15.27	2.6226767417553 4	0.2050754747936 33	97.172247783451	246.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	undefined	Y	C	thylakoid-integral	

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AT1G52400	205	AT1G52400.1	BGL1 (BETA-GLUCOSIDASE HOMOLOG 1); hydrolase, hydrolyzing O-glycosyl compounds	528	ENV	Ch/E ?	6.74	60.46	100.0	0.0	0.0	4.0	metabolism hormone ?	26.3 misc.gluco-, galacto- and mannosidases	secreted		S	-	
AT1G52510	206	AT1G52510.1	hydrolase, alpha/beta fold family protein	380	STR-ENV	Ch/E ?	6.55	41.84	22.519983469659	77.480016530341	0.0	15.0	hydrolase ?	35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT1G52670	207	AT1G52670.1	biotin/lipoyl attachment domain-containing protein	274			8.59	29.57	0.0	100.0	0.0	5.0		35.1 not assigned. no ontology	undefined	Y	C	plastid	
AT1G52740	208	AT1G52740.1	HTA9; DNA binding	134	THY-ENV	other	10.28	14.27	30.888133963744 9	9.6609675714206 2	59.450898464834 5	7.0	DNA binding	28.1.3 DNA.synthesis/chromatin structure. histone	undefined	Y		nucleus	
AT1G53180	209	AT1G53180.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15115.1)	358			9.61	40.42	0.0	100.0	0.0	3.0		35.2 not assigned. unknown	undefined			-	
AT1G53240	210	AT1G53240.1	malate dehydrogenase (NAD), mitochondrial	341	STR-ENV	other	8.53	35.8	37.213959564581	53.832750580870 1	8.953289 8545489	64.0	metabolism carbon	8.1.9 TCA / org.transformation. TCA.malate DH	undefined	Y	M	mitochondria	
AT1G53280	211	AT1G53280.1	DJ-1 family protein	438	STR		7.98	46.99	0.0	100.0	0.0	14.0		35.1 not assigned. no ontology	chloroplast	Y	C	plastid	

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AT1G53520	212	AT1G53520.1	chalcone-flavanone isomerase-related	287	STR		8.63	30.72	0.0	100.0	0.0	28.0		16.8.2 secondary metabolism.flavonoids.chalcones	undefined		C	plastid	
AT1G54040	213	AT1G54040.1	ESP (EPITHIOSPECIFIER PROTEIN)	261			5.09	28.52	0.0	100.0	0.0	3.0		17.7.3 hormone metabolism.jasmonate.induced-regulated-responsive-activated	undefined			-	
AT1G54270	214	AT1G54270.1	EIF4A-2 (eukaryotic translation initiation factor 4A-2); ATP-dependent helicase	412			5.45	46.76	0.0	0.0	100.0	2.0		29.2.3 protein.synthesis.initiation	other (e.g. cytoplasm)			-	
AT1G54500	215	AT1G54500.1	rubredoxin family protein	195	ENV-THY	Ch/E & Ch/Th	6.28	21.87	50.959095857742 8	0.0	49.040904142257 2	6.0	redox ?	29.8 protein assembly and cofactor ligation	chloroplast		C	thylakoid-integral	1.0

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AT1G54520	216	AT1G54520.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96363.1); contains InterPro domain Protein of unknown function DUF1517 (InterPro: IPR010903)	391	ENV	Ch/E/IM	9.22	42.84	100.0	0.0	0.0	2.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	2.0
AT1G54580	217	AT1G54580.1	ACP2 (ACYL CARRIER PROTEIN 2)	136			5.28	14.52	0.0	100.0	0.0	8.0		11.1.12 lipid metabolism.FA synthesis and FA elongation.ACP protein	chloroplast	Y	C	plastid	
AT1G54630	218	AT1G54630.1	ACP3 (ACYL CARRIER PROTEIN 3)	136	STR		5.28	14.65	0.0	100.0	0.0	11.0		11.1.12 lipid metabolism.FA synthesis and FA elongation.ACP protein	chloroplast	Y	C	plastid	
AT1G54780	219	AT1G54780.1	thylakoid lumen 18.3 kDa protein	285	THY	Ch/Th/Lum	8.81	31.13	6.4786253806303 6	0.0	93.521374619369 6	57.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	2.0
AT1G55450	220	AT1G55450.1	embryo-abundant protein-related	311	ENV	Ch/E ?	6.75	34.47	100.0	0.0	0.0	5.0	unknown	27.3.99 RNA.regulation of transcription.unclassified	undefined			-	1.0
AT1G55480	221	AT1G55480.1	binding / protein binding	335	THY-ENV	Ch	8.18	37.41	24.731288289538 8	3.8676369126916 4	71.401074797769 6	61.0	RNA Binding ?	35.2 not assigned. unknown	chloroplast	Y	C	thylakoid-peripheral-stromal-side	

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AT1G55490	222	AT1G55490.1	CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding / unfolded protein binding	600	STR	Ch/S	6.2	63.81	15.244794681839 2	82.741545063664 8	2.013660254496 03	1427.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT1G55670	223	AT1G55670.1	PSAG	160	THY	Ch/Th	9.56	17.08	5.555042743415 18	0.0	94.444957256584 8	162.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-integral	2.0
AT1G55930	224	AT1G55930.1	CBS domain-containing protein / transporter associated domain-containing protein	653	ENV	Ch/E/IM	5.46	72.93	100.0	0.0	0.0	16.0	transporter Mg & Co ?	35.1 not assigned. no ontology	chloroplast	Y	C	-	5.0
AT1G56050	225	AT1G56050.1	GTP-binding protein-related	421	STR		5.72	45.62	0.0	100.0	0.0	48.0		30.5 signalling.G-proteins	undefined	Y	C	plastid stroma	

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AT1G56070	226	AT1G56070.1	LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/ translation factor, nucleic acid binding	843			5.89	93.89	0.0	0.0	100.0	2.0		29.2.4 protein.synthesis.elongation	undefined			not plastid	
AT1G56190	227	AT1G56190.1	phosphoglycerate kinase, putative	478	STR	Ch/S & other	8.27	49.93	7.1945439510793 2	91.010415347416 9	1.7950407015037 7	1567.0	metabolism carbon	1.3.3 PS.calvin cyle.phosphoglycerate kinase	chloroplast	Y	C	plastid stroma	
AT1G56200	228	AT1G56200.1	EMB1303 (EMBRYO DEFECTIVE 1303)	154	ENV	Ch/E/IM	9.33	15.98	100.0	0.0	0.0	1.0	unknown	33.99 development.unspecified	chloroplast	Y	C	plastid	1.0
AT1G56500	229	AT1G56500.1	haloacid dehalogenase-like hydrolase family protein	1055	THY-STR		5.42	114.4	0.0	26.335569685153	73.664430314847	22.0		3.2 minor CHO metabolism.trehalose	chloroplast	Y	C	plastid stroma	
AT1G57770	230	AT1G57770.1	amine oxidase family	574	ENV	Ch/E/IM	6.51	61.72	100.0	0.0	0.0	5.0	metabolism vitamin and pigment ?	16.1.4 secondary metabolism.isoprenoids.carotenoids	chloroplast	Y	C	plastid	

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AT1G58080	231	AT1G58080.1	ATATP-PRT1 (ATP PHOSPHORIBOSYL TRANSFERASE)	411	STR		6.03	44.55	0.0	100.0	0.0	15.0		13.1.7.1 amino acid metabolism.synthesis.histidine.ATP phosphoribosyl transferase	chloroplast	Y	C	-	
AT1G58200	232	AT1G58200.1	MSL3 (MSCS-LIKE 3)	678	ENV	Ch/E	8.58	74.19	100.0	0.0	0.0	2.0	transporter ion channel	31.2.5 cell.division.plastid	undefined			envelope	4.0
AT1G58848	233	AT1G58848.1	ATP binding / protein binding	1049			6.85	121.04	0.0	100.0	0.0	1.0		20.1 stress.biotic	undefined			-	2.0
AT1G60000	234	AT1G60000.1	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	258			5.35	28.49	0.0	100.0	0.0	5.0		27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT1G61520	235	AT1G61520.1	LHCA3 (Photosystem I light harvesting complex gene 3); chlorophyll binding	273	THY	Ch/Th	8.61	29.18	7.9692079436695 1	0.0	92.030792056330 5	346.0	PS LHC	1.1.2.1 PS.lightreaction.photosystem I.LHC-I	chloroplast	Y	C	thylakoid-integral	
AT1G62180	236	AT1G62180.1	APR2 (5'ADENYLYLPHOSPHOSULFATE REDUCTASE 2)	454			6.45	50.65	0.0	100.0	0.0	8.0		14.2 S-assimilation.APR	chloroplast	Y	C	plastid stroma	

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AT1G62640	237	AT1G62640.1	KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-oxoacyl-[acyl-carrier-protein] synthase	404	STR		7.05	42.84	0.0	100.0	0.0	26.0		11.1.3 lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	chloroplast	Y	C	plastid stroma	1.0
AT1G62750	238	AT1G62750.1	ATSCO1/ATSCO1/CPEF-G/SCO1 (SNOWY COTYLEDON1); translation elongation factor/translation factor, nucleic acid binding	783	STR	Ch/S	5.43	86.05	1.0979532269892 3	98.902046773010 8	0.0	469.0	translation stroma	29.2.4 protein.synthesis.elongation	chloroplast	Y	C	plastid stroma	
AT1G62780	239	AT1G62780.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN83165.1)	237	STR		5.77	27.21	0.0	100.0	0.0	46.0		35.2 not assigned.unknown	chloroplast		C	plastid stroma	

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AT1G63610	240	AT1G63610.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G14910.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62022.1); similar to unknown [Populus trichocarpa] (GB:ABK95713.1)	340	STR		6.26	37.95	0.0	100.0	0.0	12.0		35.2 not assigned. unknown	chloroplast	Y	C	-	
AT1G63680	241	AT1G63680.1	ATMURE/PDE316 (PIGMENT DEFECTIVE EMBRYO); ATP binding / ligase	767			4.55	85.02	0.0	100.0	0.0	1.0		35.1 not assigned. no ontology	undefined	Y	C	-	1.0
AT1G63770	242	AT1G63770.2	peptidase M1 family protein	945	STR		6.11	106.1	0.0	100.0	0.0	96.0		29.5 protein.degradation	chloroplast	Y	C	plastid stroma	
AT1G63940	243	AT1G63940.1	monodehydroascorbate reductase, putative	486	STR		7.05	52.5	0.0	100.0	0.0	342.0		21.2.1 redox.ascorbate and glutathione.ascorbate	chloroplast	Y	C	mitochondria; plastid stroma	

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AT1G63970	244	AT1G63970.1	ISPF (Homolog of E. coli ispF (isoprenoids F)); 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	231	STR		8.94	24.81	0.0	100.0	0.0	13.0		16.1.1.5 secondary metabolism.isoprenoids.non-mevalonate pathway. MCS	chloroplast	Y	C	plastid stroma	
AT1G64190	245	AT1G64190.1	6-phosphogluconate dehydrogenase family protein	487	STR		5.33	53.37	0.0	100.0	0.0	71.0		7.1.3 OPP.oxidative PP.6-phosphogluconate dehydrogenase	secreted		S	plastid	
AT1G64510	246	AT1G64510.1	ribosomal protein S6 family protein	207			5.92	22.76	0.0	100.0	0.0	6.0		29.2.1.1.1.6 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S6	chloroplast	Y	C	plastid ribosome	
AT1G64680	247	AT1G64680.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G03055.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62908.1)	250	ENV-THY	Ch/E ?	8.52	28.16	72.837728305976 6	3.7969431452540 7	23.365328548769 4	10.0	unknown	35.2 not assigned. unknown	undefined		M	-	

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AT1G64770	248	AT1G64770.1	carbohydrate binding / catalytic	348	THY		6.38	38.0	0.0	0.0	100.0	16.0		1.1.6 PS.lightreaction.NADH DH	chloroplast		C	thylakoid	
AT1G64850	249	AT1G64850.1	calcium-binding EF hand family protein	162	ENV	Ch/E	6.11	18.09	100.0	0.0	0.0	4.0	signalling calcium ?	30.3 signalling.calcium	undefined			-	2.0
AT1G64970	250	AT1G64970.1	G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE)	348	ENV	Ch/E/IM	6.71	38.07	100.0	0.0	0.0	5.0	metabolism vitamin and pigment	16.1.3.5 secondary metabolism.isoprenoids.tocopherol biosynthesis.tocopherol methyltransferase	chloroplast	Y	C	-	
AT1G65130	251	AT1G65130.1	ubiquitin carboxyl-terminal hydrolase-related	1086			5.6	124.65	0.0	49.367597204202 1	50.632402795797 9	5.0		29.5.11 protein.degradation.ubiquitin	other (e.g. cytoplasm)			-	
AT1G65260	252	AT1G65260.1	PTAC4 (PLASTID TRANSCRIPTIONALLY ACTIVE4)	330	ENV	Ch	9.17	36.39	80.450588103517 6	14.019248771158 3	5.530163 1253241	138.0	vesicle formation	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope; plastid stroma; thylakoid-peripheral-stromal-side	
AT1G65410	253	AT1G65410.1	ATNAP11 (ARABIDOPSIS THALIANA NON-INTRINSIC ABC PROTEIN 11)	345	ENV	Ch/E/IM	7.63	37.51	100.0	0.0	0.0	8.0	transporter ABC lipids	11.15* lipid metabolism.transport	chloroplast	Y	C	envelope-inner-peripheral-stromal-side	

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AT1G65930	254	AT1G65930.1	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	410	STR		6.13	45.74	0.0	100.0	0.0	20.0		8.1.4 TCA / org.transformation.TCA.IDH	other (e.g. cytoplasm)			-	
AT1G66200	255	AT1G66200.1	ATGSR2 (Arabidopsis thaliana glutamine synthase clone R2); glutamate-ammonia ligase	356	STR		5.13	39.2	0.0	100.0	0.0	66.0		12.2.2 N-metabolism.ammonia metabolism.glutamine synthase	other (e.g. cytoplasm)			-	
AT1G66430	256	AT1G66430.1	pfkB-type carbohydrate kinase family protein	384	STR		5.54	41.47	0.0	100.0	0.0	86.0		2.2.1.1 major CHO metabolism.degradation.sucrose.fructokinase	chloroplast	Y	C	plastid stroma	
AT1G66670	257	AT1G66670.1	CLPP3 (Clp protease proteolytic subunit 3); endopeptidase Clp	309	STR-ENV	Ch/E & Ch/S	7.59	33.92	45.894448092215 7	54.105551907784 3	0.0	76.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT1G66820	258	AT1G66820.1	glycine-rich protein	109	ENV	CH/E ?	7.77	11.04	100.0	0.0	0.0	3.0	unknown	35.1.40 not assigned.no ontology.glycine rich proteins	undefined			-	2.0

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AT1G67080	259	AT1G67080.1	ABA4 (ABSCISIC ACID (ABA)-DEFICIENT 4); intramolecular oxidoreductase	220	ENV	Ch/E	9.44	24.62	100.0	0.0	0.0	7.0	unknown	16.1.4 secondary metabolism.isoprenoids.carotenoids	chloroplast	Y	C	plastid	4.0
AT1G67090	260	AT1G67090.1	RBCS1A; ribulose-bisphosphate carboxylase	180	STR-ENV	Ch & other	7.58	20.21	16.547832123725	78.014382782769 1	5.4377850935059 2	1209.0	metabolism carbon	1.3.2 PS.calvin cyle.rubisco small subunit	chloroplast	Y	C	plastid stroma	
AT1G67120	261	AT1G67120.1	midasin-related	1700			5.12	604.09	0.0	100.0	0.0	2.0		35.1 not assigned. no ontology	secreted		S	-	
AT1G67280	262	AT1G67280.1	lactoylglutathione lyase, putative / glyoxalase I, putative	350	STR		6.96	39.16	0.0	100.0	0.0	81.0		13.2.3.2 amino acid metabolism.degradation.aspartate family.threonine	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT1G67700	263	AT1G67700.1	similar to unknown [Populus trichocarpa] (GB:ABK95743.1); contains domain PTHR11804:SF2 (PTHR11804:SF2); contains domain PTHR11804 (PTHR11804)	230	ENV-THY	Ch/E ?	9.57	26.01	59.749622366825 4	0.0	40.250377633174 6	20.0	unknown	29.5 protein.degradation	undefined		M	plastid	

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AT1G67740	264	AT1G67740.1	PSBY (photosystem II BY)	189			9.56	19.46	0.0	0.0	100.0	4.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-integral	4.0
AT1G68010	265	AT1G68010.1	HPR (HYDROXYPYRUVATE REDUCTASE); glycerate dehydrogenase/ poly(U) binding	386	Mix	other	6.67	42.24	21.528679577379 4	37.034717449484 6	41.436602973136	42.0	metabolism carbon	1.2.6 PS.photorespiration.hydroxypyruvate reductase	undefined			peroxisome	
AT1G68590	266	AT1G68590.1	plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative	166	STR		9.26	18.47	0.0	100.0	0.0	17.0		29.2.1.1.1.1.83 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.PSRP3	chloroplast	Y	C	plastid ribosome	

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AT1G68660	267	AT1G68660.1	similar to unknown [Populus trichocarpa] (GB:ABK92624.1); contains InterPro domain Ribosomal protein L7/L12, C-terminal/ adaptor protein ClpS-like (InterPro: IPR014719); contains InterPro domain Adaptor protein ClpS, core (InterPro: IPR003769)	159			8.63	17.0	0.0	100.0	0.0	1.0		29.5.5 protein.degradation.serine protease	undefined	Y	C	plastid stroma	
AT1G69160	268	AT1G69160.1	unknown protein	321			8.39	36.32	0.0	100.0	0.0	1.0		35.2 not assigned. unknown	undefined			-	
AT1G69200	269	AT1G69200.1	kinase	614			5.13	68.98	0.0	100.0	0.0	3.0		2.2.1.1 major CHO metabolism.degradation.sucrose.fructokinase	undefined	Y	C	plastid	
AT1G69390	270	AT1G69390.1	ATMINE1 (ARABIDOPSIS HOMOLOGUE OF BACTERIAL MINE1); protein binding	229	ENV	Ch/E/IM	6.32	25.74	100.0	0.0	0.0	7.0	plastid division	31.2.5 cell.division.plastid	chloroplast	Y	C	envelope -inner; plastid stroma	

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AT1G69740	271	AT1G69740.1	HEMB1; porphobilinogen synthase	430	STR	Ch/E & Ch/S	6.95	46.69	6.9207842060400 1	93.07921579396	0.0	164.0	metabolism vitamin and pigment	19.4 tetrapyrrole synthesis.ALA dehydratase	chloroplast	Y	C	plastid stroma	
AT1G69830	272	AT1G69830.1	AMY3/ATAMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	887	STR		5.72	99.84	0.0	100.0	0.0	114.0		2.2.2.1 major CHO metabolism.degradation.starch.starch cleavage	chloroplast	Y	C	plastid stroma	
AT1G70570	273	AT1G70570.1	anthranilate phosphoribosyltransferase, putative	595	STR		6.43	65.22	0.0	100.0	0.0	17.0		13.1.6.5.2 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate phosphoribosyltransferase	chloroplast	Y	C	-	
AT1G70610	274	AT1G70610.1	ATTAP1 (Arabidopsis thaliana transporter associated with antigen processing protein 1); ATPase, coupled to transmembrane movement of substances	700	ENV	Ch/E/IM	8.67	78.04	100.0	0.0	0.0	43.0	transporter ABC	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope	4.0

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AT1G70710	275	AT1G70710.1	AtGH9B1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9B1); hydrolase, hydrolyzing O-glycosyl compounds	492			9.33	54.61	0.0	0.0	100.0	4.0		10.6.1 cell wall.degradation.cellulases and beta-1,4-glucanases	secreted		S	-	
AT1G70730	276	AT1G70730.1	phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	585			5.56	63.48	0.0	100.0	0.0	7.0		4.2 glycolysis.PGM	undefined	Y		-	
AT1G70820	277	AT1G70820.1	phosphoglucomutase, putative / glucose phosphomutase, putative	615	STR		5.61	67.31	0.0	100.0	0.0	40.0		4.2 glycolysis.PGM	chloroplast	Y	C	plastid stroma	

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AT1G71240	278	AT1G71240.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48840.1); similar to Os01g0869000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044923.1); similar to hypothetical protein OsJ_004118 [Oryza sativa (japonica cultivar-group)] (GB:EAZ142	824	ENV	Ch/E/IM	9.4	92.87	100.0	0.0	0.0	3.0	unknown	35.2 not assigned.unknown	undefined	Y	M	-	2.0
AT1G71500	279	AT1G71500.1	Rieske (2Fe-2S) domain-containing protein	287	THY	Ch	8.88	31.72	14.236157266974 4	3.5621460036224	82.201696729403 2	86.0	redox	26.30 misc.other Ferredoxins and Rieske domain	chloroplast	Y	C	thylakoid	
AT1G71920	280	AT1G71920.1	histidinol-phosphate aminotransferase, putative	415	STR		5.98	46.36	0.0	100.0	0.0	21.0		13.1.7.6 amino acid metabolism.synthesis.histidine.histidinol-phosphate aminotransferase	chloroplast	Y	C	-	

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AT1G72150	281	AT1G72150.1	PATL1 (PATELLIN 1); transporter	573	ENV	Ch/E & other	4.82	64.04	100.0	0.0	0.0	5.0	vesicular trafficking ?	34.99 transport.misc	undefined			-	
AT1G72250	282	AT1G72250.1	kinesin motor protein-related	1195	ENV	Ch/E ?	6.13	133.38	100.0	0.0	0.0	2.0	plastid positioning ?	31.1 cell.organisation	undefined			-	
AT1G72640	283	AT1G72640.1	binding / catalytic	312	THY-ENV	Ch/E & Ch/Th	5.55	33.63	34.191349113866 8	0.0	65.808650886133 2	3.0	protein targeting Tic ?	35.2 not assigned.unknown	chloroplast	Y	C	plastid	
AT1G72810	284	AT1G72810.1	threonine synthase, putative	516			8.23	56.92	0.0	100.0	0.0	8.0		13.1.3.2.1 amino acid metabolism.synthesis.aspartate family.threonine.threonine synthase	chloroplast	Y	C	-	
AT1G73060	285	AT1G73060.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G48790.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49401.1)	358			5.12	40.03	0.0	0.0	100.0	7.0		35.2 not assigned.unknown	chloroplast	Y	C	plastid	
AT1G73110	286	AT1G73110.1	ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative	432			6.81	48.32	0.0	32.773557540024 3	67.226442459975 7	7.0		1.3.13 PS.calvin cyle.rubisco interacting	chloroplast	Y	C	plastid	

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AT1G73990	287	AT1G73990.1	SPPA (signal peptide peptidase); protease IV/ serine-type endopeptidase	677	ENV-THY	Ch/E/IM	9.18	75.09	82.382001126792	0.0	17.617998873208	47.0	chaperone and protease	29.5 protein.degradation	chloroplast	Y	C	thylakoid-integral	
AT1G74030	288	AT1G74030.1	enolase, putative	477	STR		5.78	51.47	0.0	100.0	0.0	12.0		4.12 glycolysis.enolase	chloroplast	Y	C	plastid	
AT1G74070	289	AT1G74070.1	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	317			9.51	34.37	0.0	0.0	100.0	9.0		29.6 protein.folding	chloroplast	Y	C	-	
AT1G74260	290	AT1G74260.1	catalytic	1387	STR		5.16	151.78	0.0	100.0	0.0	22.0		23.1.2.4 nucleotide metabolism.synthesis.purine.FGAR amidotransferase	chloroplast	Y	M	mitochondria; plastid stroma	
AT1G74310	291	AT1G74310.1	ATHSP101 (HEAT SHOCK PROTEIN 101); ATP binding / ATPase	911	ENV-STR	Ch/E ?	5.8	101.29	78.246021525158 7	21.753978474841 3	0.0	17.0	chaperone and protease	20.2.1 stress.abiotic.heat	other (e.g. cytoplasm)			-	
AT1G74470	292	AT1G74470.1	geranylgeranyl reductase	467	THY	Ch/E & Ch/Th	9.03	51.83	5.5065923505446 2	0.4305780513488 36	94.062829598106 5	151.0	metabolism vitamin and pigment	16.1.1 secondary metabolism.isoprenoids.non-mevalonate pathway	chloroplast	Y	C	thylakoid	

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AT1G74640	293	AT1G74640.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO64553.1); contains domain SSF53474 (SSF53474); contains domain G3DSA:3.40.50.1820 (G3DSA:3.40.50.1820)	370	ENV	Ch/E & Ch/Th	8.3	41.05	100.0	0.0	0.0	2.0	hydrolase ?	35.2 not assigned. unknown	chloroplast	Y	C	-	
AT1G74730	294	AT1G74730.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96654.1); contains InterPro domain Protein of unknown function DUF1118 (InterPro:IPR009500)	198	THY		9.3	20.73	0.0	0.0	100.0	18.0		35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	2.0
AT1G74850	295	AT1G74850.1	PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2)	862			5.67	96.32	0.0	100.0	0.0	4.0		28.3* DNA.plastid nucleoid interacting	chloroplast	Y	C	plastid nucleoid	

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AT1G74880	296	AT1G74880.1	NDH-O (NAD(P)H:PLASTOQUINONE DEHYDROGENASE COMPLEX SUBUNIT O)	158			9.23	17.65	0.0	24.528678553158 6	75.471321446841 4	3.0		1.1.6 PS.lightreaction.NADH DH	chloroplast	Y	C	thylakoid	
AT1G74960	297	AT1G74960.1	FAB1 (FATTY ACID BIOSYNTHESIS 1); fatty-acid synthase	541	STR		8.1	57.6	0.0	100.0	0.0	29.0		11.1.3 lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	undefined	Y	C	plastid	
AT1G74970	298	AT1G74970.1	RPS9 (RIBOSOMAL PROTEIN S9); structural constituent of ribosome	208	STR-ENV	Ch/S	10.46	22.57	32.633876691768 3	67.366123308231 7	0.0	47.0	translation stroma	29.2.1.1.1.1.9 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S9	chloroplast	Y	C	plastid ribosome	
AT1G75330	299	AT1G75330.1	OTC (ORNITHINE CARBAMOYLTRANSFERASE); amino acid binding / carboxyl- or carbamoyltransferase	375	STR		7.17	41.0	0.0	100.0	0.0	29.0		13.1.2.3.21 amino acid metabolism.synthesis.glutamate family.arginine.ornithine carbamoyltransferase	chloroplast	Y	C	plastid stroma	

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AT1G75350	300	AT1G75350.1	EMB2184 (EMBRYO DEFECTIVE 2184); structural constituent of ribosome	144	Mix	Ch/S	9.81	16.03	18.165001151755 3	46.872522955263 5	34.962475892981 2	60.0	translation stroma	29.2.1.1.1.2.31 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L31	chloroplast	Y	C	plastid ribosome	
AT1G75460	301	AT1G75460.1	ATP-dependent protease La (LON) domain-containing protein	278			8.65	31.33	0.0	100.0	0.0	4.0		29.5 protein.degradation	chloroplast	Y	C	plastid	
AT1G76030	302	AT1G76030.1	(VACUOLAR ATP SYNTHASE SUBUNIT B1); hydrogen ion transporting ATP synthase, rotational mechanism	486	ENV	Ch & other	4.98	54.1	100.0	0.0	0.0	45.0	transporter ATPase	34.1.1 transport.p- and v-ATPases.H+-transporting two-sector ATPase	other (e.g. cytoplasm)			vacuole	
AT1G76080	303	AT1G76080.1	ATCDSP32/CDSP32 (CHLOROPLASTIC DROUGHT-INDUCED STRESS PROTEIN OF 32 KD); thiol-disulfide exchange intermediate	302	STR		8.65	33.68	0.0	100.0	0.0	76.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	

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AT1G76100	304	AT1G76100.1	plastocyanin	171		Lum	5.66	17.58				2.0		1.1.5.1 PS.lightreaction.other electron carrier (ox/red).plastocyanin	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT1G76140	305	AT1G76140.1	prolyl oligopeptidase	795			5.52	89.4	0.0	100.0	0.0	6.0		29.5 protein.degradation	chloroplast	Y	C	-	
AT1G76180	306	AT1G76180.1	ERD14 (EARLY RESPONSE TO DEHYDRATION 14)	185	ENV-STR	Ch/E ?	5.41	20.78	69.546741232497 8	30.453258767502 2	0.0	19.0	stress dehydration	20.2.99 stress.abiotic.unspecified	undefined			-	
AT1G76405	307	AT1G76405.2	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G20816.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66270.1)	167	ENV	Ch/E/OM	9.49	19.45	100.0	0.0	0.0	3.0	transporter ion channel	35.2 not assigned.unknown	undefined			envelope-outer	
AT1G76760	308	AT1G76760.1	ATY1 (Arabidopsis thioredoxin y1); thiol-disulfide exchange intermediate	172			9.02	19.25	0.0	100.0	0.0	3.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	

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AT1G77060	309	AT1G77060.1	mutase family protein	339	STR		6.4	36.56	0.0	100.0	0.0	24.0		27.3.99 RNA.regulation of transcription.unclassified	undefined	Y	C	plastid stroma	
AT1G77090	310	AT1G77090.1	thylakoid lumenal 29.8 kDa protein	260	THY	Lum	7.02	28.5	0.0	13.978739289650 5	86.021260710349 5	11.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-peripheral-lumenal-side	
AT1G77490	311	AT1G77490.1	TAPX; L-ascorbate peroxidase	426	THY	Ch/Th	6.8	46.09	13.805845926649 8	6.4771392446341 8	79.717014828716	22.0	stress oxidative	21.2.1 redox.ascorbate and glutathione.ascorbate	chloroplast	Y	C	thylakoid-integral	1.0
AT1G77590	312	AT1G77590.1	LACS9 (LONG CHAIN ACYL-COA SYNTHETASE 9); long-chain-fatty-acid-CoA ligase	691	ENV	Ch/E/IM	6.53	76.17	99.398384583585 1	0.0	0.601615416414 9 2	160.0	metabolism lipid	11.1.9 lipid metabolism.FA synthesis and FA elongation.long chain fatty acid CoA ligase	undefined		C	envelope-outer	
AT1G77670	313	AT1G77670.1	aminotransferase class I and II family protein	440			7.63	48.71	0.0	100.0	0.0	2.0		16.2 secondary metabolism.phenylpropanoids	undefined	Y	M	-	
AT1G78010	314	AT1G78010.1	tRNA modification GTPase, putative	560			5.19	61.12	0.0	100.0	0.0	6.0		30.5 signalling.G-proteins	undefined	Y	M	-	

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AT1G78180	315	AT1G78180.1	binding	418	ENV	Ch/E/IM	9.86	37.54	100.0	0.0	0.0	16.0	transporter MCF	34.9 transport. metabolite transporters at the mitochondrial membrane	undefined	Y		-	2.0
AT1G78370	316	AT1G78370.1	ATGSTU20 (Arabidopsis thaliana Glutathione S-transferase (class tau) 20); glutathione transferase	217			5.62	25.0	0.0	100.0	0.0	3.0		26.9 misc.glutathione S transferases	undefined		M	not plastid	
AT1G78380	317	AT1G78380.1	ATGSTU19 (GLUTATHIONE TRANSFERASE 8); glutathione transferase	219			5.79	25.65	0.0	100.0	0.0	8.0		26.9 misc.glutathione S transferases	undefined			not plastid	
AT1G78560	318	AT1G78560.1	bile acid:sodium symporter family protein	401	ENV	Ch/E/IM	9.55	42.74	100.0	0.0	0.0	4.0	transporter Na/X ?	34.14 transport. unspecified cations	chloroplast	Y	C	-	9.0
AT1G78620	319	AT1G78620.1	integral membrane family protein	333	ENV	Ch/E/IM	9.83	34.87	100.0	0.0	0.0	13.0	unknown	35.1 not assigned. no ontology	chloroplast	Y	C	-	6.0

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AT1G78630	320	AT1G78630.1	EMB1473 (EMBRYO DEFECTIVE 1473); structural constituent of ribosome	241	STR-ENV	Ch/S & Ch/Th	9.93	26.78	39.749707952277	53.874715765874 7	6.3755762818482 6	62.0	translation stroma	29.2.1.1.1.2.13 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L13	chloroplast	Y	C	plastid ribosome	
AT1G78900	321	AT1G78900.1	VHA-A; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism	623	ENV	Ch/E & other	5.11	68.81	100.0	0.0	0.0	53.0	transporter ATPase	34.1 transport.p- and v-ATPases	other (e.g. cytoplasm)			vacuole	
AT1G78915	322	AT1G78915.1	binding	385			7.66	42.58	0.0	6.1034029910058 7	93.896597008994 1	6.0		35.2 not assigned. unknown	undefined	Y	C	thylakoid	1.0
AT1G78995	323	AT1G78995.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41778.1)	159			9.2	17.15	0.0	0.0	100.0	1.0		35.2 not assigned. unknown	undefined	Y	C	-	1.0
AT1G79040	324	AT1G79040.1	PSBR (photosystem II subunit R)	140	THY	Ch/Th	9.62	14.58	4.9389632674185 2	0.0	95.061036732581 5	91.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined	Y	C	thylakoid-integral	1.0
AT1G79230	325	AT1G79230.1	ST1 (MERCAPTOPYRUVATE SULFURTRANSFERASE 1); thiosulfate sulfurtransferase	379			5.94	41.89	0.0	100.0	0.0	5.0		13.2.5.3 amino acid metabolism.degradation.serine-glycine-cysteine group.cysteine	undefined	Y	C	mitochondria	

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AT1G79440	326	AT1G79440.1	ALDH5F1 (SUCCINIC SEMIALDEHYDE DEHYDROGENASE); 3-chloroallyl aldehyde dehydrogenase/ succinate-semialdehyde dehydrogenase	528	STR		6.51	56.56	0.0	100.0	0.0	10.0		13.1.1.1.3 amino acid metabolism.synthesis.central amino acid metabolism.GABA.SSADH	undefined	Y	M	-	
AT1G79550	327	AT1G79550.1	PGK (PHOSPHOGLYCERATE KINASE)	401	STR	Ch/E ?	5.48	42.13	6.2708032949059 7	90.711817196056 8	3.0173795090372 4	246.0	metabolism carbon	4.10 glycolysis.phosphoglycerate kinase	other (e.g. cytoplasm)			-	
AT1G79560	328	AT1G79560.1	EMB1047/FTSH12 (EMBRYO DEFECTIVE 1047); ATP-dependent peptidase/ ATPase/ metalloeptidase	1008	ENV	Ch/E/IM	6.48	115.1	100.0	0.0	0.0	122.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	-	2.0
AT1G79600	329	AT1G79600.1	ABC1 family protein	711			6.35	79.02	0.0	0.0	100.0	4.0		26.56* misc.ABC1k family	chloroplast	Y	C	plastoglobules	
AT1G79790	330	AT1G79790.1	haloacid dehalogenase-like hydrolase family protein	245			4.76	27.69	0.0	100.0	0.0	5.0		35.1 not assigned. no ontology	chloroplast		C	plastid stroma	

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AT1G79850	331	AT1G79850.1	RPS17 (ribosomal protein S17); structural constituent of ribosome	149	STR-THY	Ch/S	10.57	16.28	20.654918008848 1	49.528937186528 2	29.816144804623 7	86.0	translation stroma	29.2.1.1.1.1.17 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S17	chloroplast	Y	C	plastid ribosome	
AT1G79870	332	AT1G79870.1	oxidoreductase family protein	313			5.62	34.16	0.0	100.0	0.0	7.0		26.1 misc.misc2	undefined			-	
AT1G80030	333	AT1G80030.1	DNAJ heat shock protein, putative	500	ENV	Ch/E & Ch/Th	7.48	53.82	100.0	0.0	0.0	14.0	chaperone and protease	26.29* misc.DnaJ domain with unknown function	chloroplast	Y	C	thylakoid	
AT1G80300	334	AT1G80300.1	ATNTT1; ATP:ADP antiporter	624	ENV	Ch/E/IM	9.39	68.13	100.0	0.0	0.0	48.0	transporter ATP/ADP	34.8 transport.metabolite transporters at the envelope membrane	undefined	Y	C	envelope-inner-integral	11.0
AT1G80380	335	AT1G80380.2	phosphoribulokinase/uridine kinase-related	456	STR	Ch/S	6.71	51.01	12.605365115806 5	87.394634884193 5	0.0	202.0	metabolism carbon	1.3.12 PS.calvin cyle.PRK	undefined	Y	C	plastid stroma	
AT1G80480	336	AT1G80480.1	PTAC17 (PLASTID TRANSCRIPTIONALLY ACTIVE17)	444	STR		5.67	49.48	0.0	100.0	0.0	43.0		28.3* DNA.plastid nucleoid interacting	chloroplast	Y	C	plastid stroma	

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AT1G80560	337	AT1G80560.1	3-isopropylmalate dehydrogenase, chloroplast, putative	405	STR		5.79	43.37	0.0	100.0	0.0	68.0		13.1.4.4.3 amino acid metabolism.synthesis.branched chain group.leucine specific.3-isopropylmalate dehydrogenase	undefined	Y	C	plastid stroma	
AT1G80600	338	AT1G80600.1	acetylornithine aminotransferase, mitochondrial, putative / acetylornithine transaminase, putative / AOTA, putative / ACOAT, putative	457	STR		6.36	48.82	0.0	100.0	0.0	61.0		13.1.2.3.4 amino acid metabolism.synthesis.glutamate family.arginine.acetylornithine aminotransferase	undefined		C	plastid stroma	
AT2G01140	339	AT2G01140.1	fructose-bisphosphate aldolase, putative	391	STR-THY	Ch & other	8.19	42.32	13.820974192430 2	68.444721875759 9	17.734303931809 9	189.0	metabolism carbon	1.3.6 PS.calvin cyle.aldolase	chloroplast	Y	C	plastoglobules	
AT2G01320	340	AT2G01320.1	ABC transporter family protein	725	ENV	Ch/E ?	5.71	78.9	100.0	0.0	0.0	16.0	transporter ABC	34.16 transport.ABC transporters and multidrug resistance systems	undefined			-	4.0

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AT2G01350	341	AT2G01350.1	QPT (QUINOLINATE PHOSHORIBOSYLTRANSFERASE); nicotinate-nucleotide diphosphorylase (carboxylating)	348			5.89	37.95	0.0	69.466080433718 1	30.533919566281 8	9.0		35.1 not assigned. no ontology	undefined		M	-	
AT2G02500	342	AT2G02500.1	ISPD (2-C-METHYL-D-ERYTHRITOL 4-PHOSPHATE CYTIDYLTRANSFERASE)	302	STR		5.9	33.93	0.0	100.0	0.0	39.0		16.1.1.3 secondary metabolism.isoprenoids.non-mevalonate pathway. CMS	undefined	Y	M	plastid stroma	
AT2G02590	343	AT2G02590.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41025.1); contains InterPro domain Putative small multi-drug export (InterPro: IPR009577)	324	ENV	Ch/E/IM	10.04	35.52	100.0	0.0	0.0	3.0	transporter multidrug?	34 transport	chloroplast	Y	C	-	6.0
AT2G02740	344	AT2G02740.1	ATWHY3/PTAC11 (A. THALIANA WHIRLY 3); DNA binding	268	STR		9.53	29.72	0.0	100.0	0.0	11.0		27.3.82 RNA.regulation of transcription.plant TF (pbf2)	undefined	Y	C	plastid nucleoid	1.0

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AT2G03420	345	AT2G03420.1	similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABF94594.1); similar to hypothetical protein OsI_010237 [Oryza sativa (indica cultivar-group)] (GB:EAY89004.1)	170			8.63	19.02	0.0	0.0	100.0	3.0		35.2 not assigned. unknown	undefined	Y	C	-	
AT2G04030	346	AT2G04030.1	CR88 (EMBRYO DEFECTIVE 1956); ATP binding	780	STR		4.93	88.66	0.0	100.0	0.0	331.0		29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT2G04039	347	AT2G04039.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41070.1)	199			6.15	21.41				1.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid	
AT2G04350	348	AT2G04350.1	long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8)	720	ENV	Ch/E ?	7.5	78.34	100.0	0.0	0.0	16.0	metabolism lipid	11.1.9 lipid metabolism.FA synthesis and FA elongation.long chain fatty acid CoA ligase	other (e.g. cytoplasm)			-	1.0

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AT2G04400	349	AT2G04400.1	indole-3-glycerol phosphate synthase (IGPS)	402	STR		6.98	44.57	0.0	100.0	0.0	31.0		13.1.6.5.4 amino acid metabolism.synthesis.aromatic aa.tryptophan.indole-3-glycerol phosphate synthase	undefined	Y	C	plastid stroma	
AT2G04700	350	AT2G04700.1	ferredoxin thioredoxin reductase catalytic beta chain family protein	146	STR-ENV	Ch/E ?	8.11	16.43	19.739259549333 5	80.260740450666 5	0.0	14.0	redox	21.1 redox.thioredoxin	chloroplast	Y	C	-	
AT2G04842	351	AT2G04842.1	EMB2761 (EMBRYO DEFECTIVE 2761); threonine-tRNA ligase	650	STR		6.47	74.78	0.0	100.0	0.0	22.0		29.1.3 protein.aa activation.threonine-tRNA ligase	chloroplast	Y	C	mitochondria; plastid stroma	
AT2G05070	352	AT2G05070.1	LHCB2.2 (Photosystem II light harvesting complex gene 2.2); chlorophyll binding	265	THY	Ch/Th	5.28	28.62	1.0631052665910 8	0.720439180780422	98.216455552628 5	965.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0

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AT2G05620	353	AT2G05620.1	PGR5 (PROTON GRADIENT REGULATION 5)	133	THY	Ch/Th	10.65	14.29	11.495751735268 5	0.0	88.504248264731 5	36.0	PS PSI cyclic electron flows	1.1.40 PS.lightreaction.cyclic electron flow-chlororespiration	undefined	Y		thylakoid-peripheral-stromal-side	
AT2G05710	354	AT2G05710.1	aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	990	STR		6.72	108.2	0.0	100.0	0.0	27.0		8.2.3 TCA / org.transformation.other organic acid transformaitons.aconitase	chloroplast	Y	C	plastid stroma	
AT2G05990	355	AT2G05990.1	MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase	390	STR	Ch	9.09	41.21	3.6457364899419 5	96.354263510058	0.0	206.0	metabolism lipid	11.1.6 lipid metabolism.FA synthesis and FA elongation.enoyl ACP reductase	chloroplast	Y	C	plastid stroma	2.0
AT2G07698	356	AT2G07698.1	ATP synthase alpha chain, mitochondrial, putative	777	THY	Ch/E & other	5.43	85.93	13.921437340825 3	10.159908915032 8	75.918653744141 9	113.0	transporter ATPase	9.9 mitochondrial electron transport / ATP synthesis .F1-ATPase	secreted	Y	S	-	3.0
AT2G12550	357	AT2G12550.1	ubiquitin-associated (UBA)/TS-N domain-containing protein	562			4.9	62.08	0.0	0.0	100.0	7.0		29.5.11 protein.degradation.ubiquitin	undefined			-	

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AT2G13360	358	AT2G13360.1	AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE)	401	STR		7.68	44.2	0.0	100.0	0.0	15.0		1.2.3 PS.aminotransferases peroxisomal	undefined			peroxisome	
AT2G14880	359	AT2G14880.1	SWIB complex BAF60b domain-containing protein	141			9.87	15.9	0.0	0.0	100.0	6.0		35.1 not assigned. no ontology	chloroplast	Y	C	-	
AT2G15290	360	AT2G15290.1	ATTIC21/CIA5/PIC1/TIC21 (CHLOROPLAST IMPORT APPARATUS 5); copper uptake transmembrane transporter/ iron ion transmembrane transporter/ protein homodimerization	296	ENV	Ch/E/IM	10.23	31.27	92.173207954625 4	0.0	7.8267920453746 3	37.0	protein targeting Tic ? Transporter Iron ?	34.12 transport. metal	chloroplast	Y	C	envelope-inner-integral	4.0
AT2G15620	361	AT2G15620.1	NIR1 (NITRITE REDUCTASE); ferredoxin-nitrate reductase	586	STR	Ch & other	5.95	65.5	2.5605557522408 6	97.439444247759 1	0.0	505.0	redox	12.1.2 N-metabolism.nitrate metabolism.nitrite reductase	chloroplast	Y	C	plastid stroma	
AT2G16070	362	AT2G16070.2	PDV2 (PLASTID DIVISION2)	224	ENV	Ch/E/OM	9.16	24.77	100.0	0.0	0.0	8.0	plastid division	31.2.5 cell.division.plastid	other (e.g. cytoplasm)		M	envelope	1.0

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AT2G16640	363	AT2G16640.1	ATTOC132/TOC132 (MULTIMERIC TRANSLOCON COMPLEX IN THE OUTER ENVELOPE MEMBRANE 132); transmembrane receptor	1206	ENV	Ch/E/OM	4.75	132.27	100.0	0.0	0.0	2.0	protein targeting Toc	29.3.3 protein.targeting.chloroplast	other (e.g. cytoplasm)			envelope-outer	
AT2G17265	364	AT2G17265.1	HSK (HOMOSERINE KINASE); homoserine kinase	370	STR		8.51	38.52	0.0	100.0	0.0	20.0		13.1.3.6.1.4 amino acid metabolism.synthesis.aspartate family.misc.homoserine.homoserine kinase	chloroplast	Y	C	plastid	
AT2G17390	365	AT2G17390.1	AKR2B; protein binding / transcription regulator	344			4.37	36.89	0.0	100.0	0.0	1.0		27.3.39 RNA.regulation of transcription.AtSR Transcription Factor family	undefined			-	
AT2G17630	366	AT2G17630.1	phosphoserine aminotransferase, putative	422	STR-THY		8.26	46.63	0.0	76.470954340705 9	23.529045659294 1	38.0		13.1.5.1.2 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoserine aminotransferase	chloroplast	Y	C	-	

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AT2G17695	367	AT2G17695.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO40657.1)	205	ENV	Ch/E ?	9.2	23.24	100.0	0.0	0.0	17.0	unknown	35.2 not assigned. unknown	undefined		M	-	
AT2G18020	368	AT2G18020.1	EMB2296 (EMBRYO DEFECTIVE 2296); structural constituent of ribosome	258			10.91	27.86	0.0	100.0	0.0	3.0		29.2.1.2.2.8 Protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L8	undefined		M	cytosol	
AT2G18710	369	AT2G18710.1	SCY1 (SECY HOMOLOG 1); P-P-bond-hydrolysis-driven protein transmembrane transporter	551			9.49	59.49	0.0	0.0	100.0	3.0		29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	thylakoid-integral	10.0
AT2G19940	370	AT2G19940.1	semialdehyde dehydrogenase family protein	359	STR		6.5	39.6	0.0	100.0	0.0	124.0		13.1.2.3 amino acid metabolism.synthesis.glutamate family.arginine	chloroplast			plastid stroma	
AT2G20260	371	AT2G20260.1	PSAE-2 (photosystem I subunit E-2); catalytic	145	THY-ENV	Ch/Th	9.94	15.18	20.884700267079	2.3753330148300 9	76.739966718090 9	125.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT2G20270	372	AT2G20270.1	glutaredoxin family protein	179	STR		8.36	19.12	0.0	100.0	0.0	10.0		21.4 redox.glutaredoxins	chloroplast	Y	C	plastid stroma	

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AT2G20690	373	AT2G20690.1	lumazine-binding family protein	271			7.62	29.64	0.0	100.0	0.0	8.0		18.3.2 Co-factor and vitamine metabolism.riboflavin.riboflavin synthase	chloroplast	Y	C	plastid	
AT2G20890	374	AT2G20890.1	PSB29 (THYLAKOID FORMATION1)	300	THY-ENV	Ch	9.2	33.79	27.162980892588 3	1.5446983789628 5	71.292320728448 9	106.0	vesicle formation	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope; plastid stroma; thylakoid-peripheral-stromal-side	
AT2G21170	375	AT2G21170.1	TIM (TRIOSE PHOSPHATE ISOMERASE); triose-phosphate isomerase	315	STR	Ch/S & other	7.67	33.34	6.8466814456042 1	93.153318554395 8	0.0	285.0	metabolism carbon	1.3.5 PS.calvin cycle.TPI	chloroplast	Y	C	plastid stroma	
AT2G21195	376	AT2G21195.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO44591.1)	93	ENV	CH/E ?	8.93	10.36	100.0	0.0	0.0	1.0	unknown	35.2 not assigned. unknown	other (e.g. cytoplasm)			-	
AT2G21280	377	AT2G21280.1	GC1 (GIANT CHLOROPLAST 1); binding / catalytic/ coenzyme binding	347	ENV	Ch/E/IM	9.31	37.74	86.656816262335 8	0.0	13.343183737664 2	33.0	plastid division	31.2.5 cell.division.plastid	chloroplast	Y	C	envelope-inner-peripheral-stromal-side	
AT2G21330	378	AT2G21330.1	fructose-bisphosphate aldolase, putative	399	STR-THY	Ch	6.17	42.93	14.719971435226 3	68.753162353527 5	16.526866211246 2	827.0	metabolism carbon	1.3.6 PS.calvin cyle.aldolase	chloroplast	Y	C	plastid stroma; plastoglobules	

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AT2G21340	379	AT2G21340.1	enhanced disease susceptibility protein, putative / salicylic acid induction deficient protein, putative	555	ENV	Ch/E/IM	7.49	59.74	100.0	0.0	0.0	13.0	transporter multidrug?	34 transport	chloroplast	Y	C	-	9.0
AT2G21370	380	AT2G21370.1	xylulose kinase, putative	478			6.36	52.46	0.0	100.0	0.0	2.0		3.7 minor CHO metabolism.sugar kinases	undefined	Y	M	plastid	
AT2G21385	381	AT2G21385.1	similar to Os09g0531100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063753.1); similar to unknown [Picea sitchensis] (GB:ABK27019.1)	330	STR		7.02	37.55	0.0	100.0	0.0	15.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT2G21530	382	AT2G21530.1	forkhead-associated domain-containing protein / FHA domain-containing protein	209	STR		7.73	22.67	0.0	100.0	0.0	26.0		35.1 not assigned. no ontology	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	

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AT2G21660	383	AT2G21660.1	ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	176	THY	other	5.85	16.89	8.6311509957500 6	0.0	91.368849004249 9	32.0	RNA Binding	27.4 RNA.RNA binding	undefined			not plastid	
AT2G21960	384	AT2G21960.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G56180.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71767.1)	332	THY		8.83	35.8	0.0	0.0	100.0	15.0		35.2 not assigned. unknown	undefined	Y	C	plastid	3.0
AT2G22230	385	AT2G22230.1	beta-hydroxyacyl-ACP dehydratase, putative	220	THY		8.6	24.24	0.0	0.0	100.0	16.0		11.1.5 lipid metabolism.FA synthesis and FA elongation.beta hydroxyacyl ACP dehydratase	chloroplast	Y	C	plastid	

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AT2G22250	386	AT2G22250.1	AAT/ATAAT/MEE17 (maternal effect embryo arrest 17); aspartate transaminase	428	STR		6.18	46.03	0.0	100.0	0.0	28.0		13.1.1.2.1 amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	chloroplast	Y	C	plastid	
AT2G22360	387	AT2G22360.1	DNAJ heat shock family protein	442	ENV	Ch/E & Ch/Th	9.24	47.76	89.502294413689 9	10.497705586310 1	0.0	11.0	chaperone and protease	26.29* misc.DnaJ domain with unknown function	undefined	Y	C	thylakoid	
AT2G22450	388	AT2G22450.1	riboflavin biosynthesis protein, putative	476			5.8	52.2	0.0	100.0	0.0	5.0		18.3.1 Co-factor and vitamine metabolism.riboflavin.GTP cyclohydrolase II	undefined	Y		plastid	
AT2G22560	389	AT2G22560.1	kinase interacting protein-related	891			4.96	101.46				1.0		29.4.1 protein.postranslational modification.kinase	undefined			-	
AT2G22910	390	AT2G22910.1	GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein	609			7.11	67.18	0.0	100.0	0.0	4.0		26.24 misc.GCN5-related N-acetyltransferase	undefined			-	

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AT2G23670	391	AT2G23670.1	YCF37 (Arabidopsis homolog of Synechocystis YCF37)	167	THY		6.75	17.07	0.0	0.0	100.0	10.0		35.1 not assigned. no ontology	chloroplast	Y	C	thylakoid	1.0
AT2G23820	392	AT2G23820.1	metal-dependent phosphohydrolase HD domain-containing protein	245			5.8	26.93	0.0	100.0	0.0	2.0		35.1 not assigned. no ontology	undefined	Y	M	-	
AT2G24020	393	AT2G24020.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G30620.1); similar to unknown [Picea sitchensis] (GB:ABK26000.1); similar to Os02g0180200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046090.1); contains InterPro domain Conserved hypo	182	STR-ENV	Ch/S & Ch/Th	9.13	19.81	21.648639597516 2	78.351360402483 8	0.0	109.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	

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AT2G24060	394	AT2G24060.1	translation initiation factor 3 (IF-3) family protein	312			5.77	35.14	0.0	0.0	100.0	6.0		29.2.3 protein.synthesis.initiation	chloroplast	Y	C	-	
AT2G24090	395	AT2G24090.1	ribosomal protein L35 family protein	145			11.83	16.08	0.0	100.0	0.0	3.0		29.2.1.1.3.2.35 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L35	chloroplast	Y	C	plastid ribosome	
AT2G24200	396	AT2G24200.1	cytosol aminopeptidase	520	STR		5.65	54.51	0.0	100.0	0.0	73.0		29.5 protein.degradation	other (e.g. cytoplasm)			not plastid	
AT2G24270	397	AT2G24270.1	ALDH11A3 (Aldehyde dehydrogenase 11A3); 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+)	496			6.22	53.06	0.0	100.0	0.0	7.0		1.3.4 PS.calvincyle.GAP	other (e.g. cytoplasm)			cytosol	

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AT2G24820	398	AT2G24820.1	TIC55 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 55); oxidoreductase	539	ENV	Ch/E/IM	8.94	60.6	100.0	0.0	0.0	268.0	protein targeting Tic	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope-inner-integral	2.0
AT2G25080	399	AT2G25080.1	ATGPX1 (GLUTATHIONE PEROXIDASE 1); glutathione peroxidase	236	Mix	Ch/E & Ch/Th	9.41	26.01	33.746945938571 8	33.776403661517 8	32.476650399910 5	29.0	stress oxidative	21.2.2 redox.ascorbate and glutathione.glutathione	chloroplast	Y	C	plastid stroma	
AT2G25140	400	AT2G25140.1	CLPB-M/CLPB4/HSP98.7 (HEAT SHOCK PROTEIN 98.7); ATP binding / ATPase	964	ENV-STR	Ch/E/IM	6.53	108.66	58.246357331859 7	34.567250356395 2	7.186392311745 0 9	141.0	chaperone and protease	29.6 protein.folding	undefined	Y	M	-	
AT2G25730	401	AT2G25730.1	binding / heme binding	2464			5.65	274.77	0.0	0.0	100.0	1.0		26.33* misc.tetratricopeptide repeat (TPR) unknown function	undefined			-	2.0
AT2G25840	402	AT2G25840.1	OVA4 (OVULE ABORTION 4); ATP binding / aminoacyl-tRNA ligase	408	STR		8.28	45.3	0.0	88.636568577354 3	11.363431422645 7	27.0		29.1 protein.aa activation	chloroplast	Y	C	mitochondria; plastid stroma	

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AT2G26340	403	AT2G26340.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO43885.1)	253			6.74	25.34	0.0	0.0	100.0	4.0		35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	
AT2G26540	404	AT2G26540.1	HEMD; uroporphyrinogen-III synthase	321			7.8	34.22				2.0		19.6 tetrapyrrole synthesis .uroporphyrinogen III synthase	chloroplast	Y	C	plastid	
AT2G26670	405	AT2G26670.1	HY1 (HEME OXYGENASE 1)	282			6.5	32.69	0.0	100.0	0.0	5.0		19.21 tetrapyrrole synthesis .heme oxygenase	chloroplast	Y	C	plastid	
AT2G26900	406	AT2G26900.1	bile acid:sodium symporter family protein	409	ENV-THY	Ch/E/IM	8.95	43.6	71.835371943776	0.0	28.164628056224	40.0	transporter Na/X ?	34.8 transport. metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	9.0
AT2G26930	407	AT2G26930.1	ATCDPMEK (PIGMENT DEFECTIVE 277); 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	383			6.55	42.04	0.0	100.0	0.0	8.0		16.1.1.4 secondary metabolism.isoprenoids.non-mevalonate pathway. CMK	chloroplast	Y	C	-	

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AT2G27290	408	AT2G27290.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO48682.1); contains InterPro domain Protein of unknown function DUF1279 (InterPro:IPR009688)	201			9.19	21.76	0.0	0.0	100.0	1.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid	1.0
AT2G27490	409	AT2G27490.1	ATCOAE; ATP binding / dephospho-CoA kinase	232	ENV	Ch/E ?	9.54	25.74	100.0	0.0	0.0	2.0	coenzyme A biosynthesis	35.1 not assigned. no ontology	undefined			-	
AT2G27680	410	AT2G27680.1	aldo/keto reductase family protein	384	Mix	Ch/E/IM	8.2	43.15	16.766670887230 4	40.205213540188 7	43.028115572580 9	44.0	redox ?	3.5 minor CHO metabolism.others	chloroplast	Y	C	plastid stroma	
AT2G27710	411	AT2G27710.1	60S acidic ribosomal protein P2 (RPP2B)	115	ENV	Ch/E & other	4.66	11.44	100.0	0.0	0.0	1.0	translation cytosol	29.2.1.2.2.82 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P2	secreted		S	cytosol	
AT2G28000	412	AT2G28000.1	CPN60A (chloroplast / 60 kDa chaperonin alpha subunit); ATP binding / protein binding / unfolded protein binding	586	STR-ENV	Ch & other	5.08	62.07	17.351402747503 7	82.269091233300 8	0.379506019195491	1195.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	

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AT2G28050	413	AT2G28050.1	pentatricopeptide (PPR) repeat-containing protein	462			5.44	52.93	0.0	100.0	0.0	9.0		35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	undefined	Y		-	1.0
AT2G28190	414	AT2G28190.1	CSD2 (COPPER/ZINC SUPEROXIDE DISMUTASE 2); copper, zinc superoxide dismutase	216	STR	Ch/S	6.48	22.24	13.213131871372 5	86.786868128627 5	0.0	36.0	stress oxidative	21.6 redox.dismutases and catalases	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT2G28800	415	AT2G28800.1	ALB3 (ALBINO 3); P-P-bond-hydrolysis-driven protein transmembrane transporter	462	THY		9.08	50.24	0.0	0.0	100.0	16.0		29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	thylakoid-integral	4.0
AT2G28900	416	AT2G28900.1	OEP16 (OUTER ENVELOPE PROTEIN 16); P-P-bond-hydrolysis-driven protein transmembrane transporter	148	ENV	Ch/E & other	9.16	15.48	90.499004401724 5	0.0	9.500995982754 7	198.0	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane	undefined			envelope-outer	

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AT2G29630	417	AT2G29630.1	thiamine biosynthesis family protein / thiC family protein	644	STR		5.99	71.98	0.0	100.0	0.0	19.0		18.2 Co-factor and vitamine metabolism.thiamine	chloroplast	Y	C	plastid stroma	
AT2G29650	418	AT2G29650.1	inorganic phosphate transporter, putative	512	ENV	Ch/E/IM	9.0	56.49	100.0	0.0	0.0	3.0	transporter Pi ?	34.7 transport.phosphate	chloroplast	Y	C	envelope-inner-integral	9.0
AT2G29690	419	AT2G29690.1	ASA2 (anthranilate synthase 2); anthranilate synthase	621			6.25	69.81	0.0	100.0	0.0	8.0		13.1.6.5.1 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate synthase	chloroplast	Y	C	plastid stroma	
AT2G29720	420	AT2G29720.1	CTF2B; monooxygenase	427	ENV-THY	CH/E ?	9.52	46.88	50.959095857742 8	0.0	49.040904142257 2	2.0	redox ?	26.7 misc.oxidases - copper, flavone etc.	mitochondrion		M	-	
AT2G30170	421	AT2G30170.1	catalytic	298	STR		5.11	32.28	0.0	100.0	0.0	11.0		35.2 not assigned. unknown	undefined		C	plastid; plastid	
AT2G30200	422	AT2G30200.1	[acyl-carrier-protein] S-malonyltransferase/ binding / catalytic/ transferase	393	STR	Ch/E & Ch/S	8.72	41.52	3.7091794341919 3	96.290820565808 1	0.0	121.0	metabolism lipid	11.1.2 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Transacylase	chloroplast	Y	C	plastid stroma	
AT2G30390	423	AT2G30390.1	ferrochelatase II	512			5.21	56.62	0.0	0.0	100.0	4.0		19.20 tetrapyrrole synthesis.ferrochelatase	chloroplast	Y	C	-	

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AT2G30695	424	AT2G30695.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO46271.1); contains InterPro domain Trigger factor, ribosome-binding, bacterial; (InterPro:IPR008881)	199	STR		6.32	22.26	0.0	100.0	0.0	11.0		29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT2G30790	425	AT2G30790.1	PSBP-2 (photosystem II subunit P-2); calcium ion binding	261	THY-STR	Ch/Th/Lum	9.0	28.18	3.3263126307377 1	16.646080851984 3	80.027606517278	76.0	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT2G30860	426	AT2G30860.1	ATGSTF9 (Arabidopsis thaliana Glutathione S-transferase (class phi) 9); glutathione transferase	215			6.16	24.14	0.0	100.0	0.0	4.0		26.9 misc.glutathione S transferases	undefined			not plastid	
AT2G30930	427	AT2G30930.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G06540.1)	164	ENV	Ch/E & other	4.92	16.93	100.0	0.0	0.0	5.0	unknown	35.2 not assigned. unknown	undefined		C	-	

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AT2G30950	428	AT2G30950.1	VAR2 (VARIEGATED 2); ATP-dependent peptidase/ ATPase/ metallopeptidase/ zinc ion binding	695	THY	Ch/E & Ch/Th/Lum	5.99	74.15	10.350655504659 6	0.0	89.649344495340 4	352.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	thylakoid-integral	1.0
AT2G31040	429	AT2G31040.1	ATP synthase protein I - related	350			9.27	38.61	0.0	0.0	100.0	4.0		1.1.4 PS.lightreaction.ATP synthase	chloroplast		C	-	2.0
AT2G31170	430	AT2G31170.1	tRNA synthetase class I (C) family protein	563	STR		6.75	63.91	0.0	100.0	0.0	17.0		29.1.16 protein.aa activation.cysteine-tRNA ligase	chloroplast	Y	C	mitochondria; plastid stroma	

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AT2G31190	431	AT2G31190.1	similar to EMB1879 (EMBRYO DEFECTIVE 1879) [Arabidopsis thaliana] (TAIR:AT5G49820.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40639.1); contains InterPro domain Protein of unknown function DUF647 (InterPro:IPR006968)	433	ENV	CH/E ?	7.7	48.25	100.0	0.0	0.0	7.0	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	2.0
AT2G31610	432	AT2G31610.1	40S ribosomal protein S3 (RPS3A)	250	ENV	Ch & other	9.56	27.52	100.0	0.0	0.0	3.0	translation cytosol	29.2.1.2.1.3 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S3	undefined			cytosol	

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AT2G31670	433	AT2G31670.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G51360.1); similar to unknown [Populus trichocarpa] (GB:ABK93857.1); contains InterPro domain Dimeric alpha-beta barrel (InterPro:IPR011008); contains InterPro domain Stress responsive alpha-	263	STR		6.44	28.86	0.0	100.0	0.0	27.0		35.2 not assigned. unknown	undefined	Y	M	plastid stroma	
AT2G31810	434	AT2G31810.1	acetolactate synthase small subunit, putative	491			9.07	53.87	0.0	100.0	0.0	7.0		13.1.4.1.1 amino acid metabolism.synthesis.branched chain group.common.acetolactate synthase	chloroplast	Y	C	-	
AT2G32290	435	AT2G32290.1	BAM6/BMY5 (BETA-AMYLASE 6); beta-amylase	577	ENV	Ch/S	6.32	66.56	100.0	0.0	0.0	6.0	metabolism carbon	2.2.2.1 major CHO metabolism.degradation.starch.starch cleavage	undefined			-	

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AT2G32760	436	AT2G32760.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO50091.1); contains domain PTHR15157 (PTHR15157); contains domain PTHR15157:SF2 (PTHR15157:SF2)	352			8.56	39.91	0.0	100.0	0.0	1.0		35.2 not assigned. unknown	undefined			-	
AT2G33210	437	AT2G33210.1	chaperonin, putative	585	STR-ENV	Ch/E & other	6.37	61.97	27.333093838892 5	72.666906161107 5	0.0	36.0	chaperone and protease	29.6 protein.folding	undefined		M	mitochondria	
AT2G33430	438	AT2G33430.1	plastid developmental protein DAG, putative	219			8.51	24.71	0.0	100.0	0.0	5.0		29.2.7* protein.synthesis.ribosome biogenesis	undefined	Y	M	plastid	
AT2G33450	439	AT2G33450.1	50S ribosomal protein L28, chloroplast (CL28)	143	STR-ENV	Ch/S	11.17	16.03	26.212628759875	73.787371240125	0.0	11.0	translation stroma	29.2.1.1.1.2.28 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L28	undefined	Y	C	plastid ribosome	
AT2G33800	440	AT2G33800.1	ribosomal protein S5 family protein	303	STR-THY	Ch & other	8.99	32.64	15.225724094869 1	62.409780333599 3	22.364495571531 5	414.0	translation stroma	29.2.1.1.1.1.5 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S5	chloroplast	Y	C	plastid ribosome	

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AT2G34420	441	AT2G34420.1	LHB1B2 (Photosystem II light harvesting complex gene 1.5); chlorophyll binding	265	THY	Ch/Th	5.28	28.05	1.3796495755732 7	0.7012148570037 03	97.919135567423	1007.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0
AT2G34430	442	AT2G34430.1	LHB1B1 (Photosystem II light harvesting complex gene 1.4); chlorophyll binding	266	THY	Ch/Th	5.15	28.17	1.0612956017941 8	0.7192128173479 93	98.219491580857 8	980.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	undefined	Y	C	thylakoid-integral	2.0
AT2G34460	443	AT2G34460.1	flavin reductase-related	280	ENV-THY	Ch/E & Ch/Th	9.03	30.47	84.101838560808 8	0.0	15.898161439191 2	74.0	protein targeting Tic ?	35.1 not assigned. no ontology	undefined	Y	C	plastoglobules	
AT2G34585	444	AT2G34585.1	similar to unknown [Populus trichocarpa] (GB:ABK92885.1)	81	ENV	Ch/E & other	4.03	8.57	100.0	0.0	0.0	2.0	unknown	35.2 not assigned. unknown	secreted		S	-	
AT2G35040	445	AT2G35040.1	AICARFT/IMPCHase bienzyme family protein	596	STR		6.45	64.9	0.0	100.0	0.0	44.0		23.1.2.9 nucleotide metabolism.synthesis.purine.AICAR transformylase and IMP synthase	chloroplast	Y	C	plastid stroma	

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AT2G35410	446	AT2G35410.1	33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative	308	STR		5.55	33.78	0.0	91.811821337753 6	8.1881786622464 3	82.0		27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT2G35490	447	AT2G35490.1	plastid-lipid associated protein PAP, putative	376	THY	Ch	4.45	40.5	4.9448343682498 6	4.6398287964349 5	90.415336835315 2	60.0	PAP_fibrillin	26.31* misc.fibrillins	chloroplast	Y	C	plastoglobules; thylakoid-peripheral-stromal-side	
AT2G35500	448	AT2G35500.1	shikimate kinase-related	387			5.89	42.68	0.0	100.0	0.0	3.0		13.1.6.1.5 amino acid metabolism.synthesis.aromatic aa.chorismate.shikimate kinase	chloroplast	Y	C	plastid stroma	
AT2G35800	449	AT2G35800.1	mitochondrial substrate carrier family protein	823	ENV	Ch/E ?	8.95	90.62	100.0	0.0	0.0	38.0	transporter MCF	34.9 transport.metabolite transporters at the mitochondrial membrane	undefined			-	2.0

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AT2G36145	450	AT2G36145.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO15876.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN74693.1)	186			9.32	19.9	0.0	100.0	0.0	9.0		35.2 not assigned.unknown	undefined	Y	C	thylakoid	
AT2G36160	451	AT2G36160.1	40S ribosomal protein S14 (RPS14A)	150	ENV	Ch & other	10.6	16.25	94.112814640324 4	5.8871853596756 3	0.0	6.0	translation cytosol	29.2.1.2.1.14 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S14	other (e.g. cytoplasm)			cytosol	
AT2G36230	452	AT2G36230.1	APG10 (ALBINO AND PALE GREEN 10); 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	304			6.55	33.36	0.0	100.0	0.0	6.0		13.1.7.4 amino acid metabolism.synthesis.histidine.N-5-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase	undefined	Y	M	-	
AT2G36250	453	AT2G36250.1	FTSZ2-1 (FtsZ homolog 2-1); structural molecule	478	THY-STR		5.55	50.72	0.0	42.484157314346	57.515842685654	44.0		31.2.5 cell.division.plastid	undefined		C	plastid stroma	

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AT2G36390	454	AT2G36390.1	SBE2.1 (STARCH BRANCHING ENZYME 2.1); 1,4-alpha-glucan branching enzyme	858			5.34	97.66	0.0	100.0	0.0	8.0		2.1.2.3 major CHO metabolism.synthesis.starch.starch branching	chloroplast	Y	C	plastid stroma	
AT2G36460	455	AT2G36460.1	fructose-bisphosphate aldolase, putative	358			7.01	38.38	0.0	100.0	0.0	5.0		4.7 glycolysis.aldolase	undefined			cytosol	
AT2G36530	456	AT2G36530.1	LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase	444			5.54	47.72	0.0	100.0	0.0	6.0		4.12 glycolysis.enolase	undefined			cytosol	1.0
AT2G36830	457	AT2G36830.1	GAMMA-TIP (Tonoplast intrinsic protein (TIP) gamma); water channel	251	ENV	Ch/E & other	6.02	25.62	100.0	0.0	0.0	6.0	transporter aquaporin	34.19.2 transport.Major Intrinsic Proteins.TIP	undefined			-	7.0
AT2G36835	458	AT2G36835.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN81061.1)	124	ENV	Ch/E/IM	7.84	13.38	100.0	0.0	0.0	10.0	unknown	35.2 not assigned.unknown	undefined		C	-	

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AT2G36885	459	AT2G36885.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO63025.1)	256			6.37	27.49	0.0	0.0	100.0	5.0		35.2 not assigned. unknown	chloroplast	Y	C	-	5.0
AT2G37020	460	AT2G37020.1	DNA binding	238	STR		5.35	27.32	0.0	100.0	0.0	12.0		35.1 not assigned. no ontology	chloroplast			-	
AT2G37080	461	AT2G37080.1	myosin heavy chain-related	583			5.17	65.85	0.0	100.0	0.0	5.0		31.1 cell.organisation	chloroplast	Y	C	-	
AT2G37190	462	AT2G37190.1	60S ribosomal protein L12 (RPL12A)	166	ENV	Ch/E & other	9.05	17.94	86.476285785767 9	13.523714214232 1	0.0	9.0	translation cytosol	29.2.1.2.2.12 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L12	undefined			cytosol	
AT2G37220	463	AT2G37220.1	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	289	STR-THY	Ch	5.05	30.71	12.479297858528 3	52.692993461582 6	34.827708679889 1	239.0	RNA Binding	27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT2G37230	464	AT2G37230.1	pentatricopeptide (PPR) repeat-containing protein	757	THY	Ch/Th	8.89	85.7	4.5102173319537 4	0.0	95.4897826680462	48.0	unknown	26.54* misc.pentatricopeptide (PPR) repeat-containing protein	mitochondrion	Y	M	-	
AT2G37400	465	AT2G37400.1	chloroplast lumen common family protein	333	ENV	Ch/E/IM	6.7	38.15	100.0	0.0	0.0	18.0	unknown	35.1 not assigned. no ontology	undefined	Y	C	-	

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AT2G37500	466	AT2G37500.1	arginine biosynthesis protein ArgJ family	468	STR		6.21	48.71	0.0	100.0	0.0	23.0		13.1.2.3.2 amino acid metabolism.synthesis.glutamate family.arginine.acetylglutamate kinase	undefined	Y	C	plastid stroma	
AT2G37660	467	AT2G37660.1	binding / catalytic/ coenzyme binding	325	STR	Ch/E & Ch/S	8.37	34.88	5.2588090790094 2	94.741190920990 6	0.0	353.0	protein targeting Tic ?	35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT2G37690	468	AT2G37690.1	phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative	642	STR		6.52	69.75	0.0	100.0	0.0	15.0		23.1.2.6 nucleotide metabolism.synthesis.purine.AIR carboxylase	undefined	Y	C	plastid	
AT2G37860	469	AT2G37860.3	LCD1 (LOWER CELL DENSITY 1)	347	ENV	Ch/E/IM	5.57	37.35	100.0	0.0	0.0	35.0	unknown	33.99 development.unspecified	undefined	Y	C	-	2.0

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AT2G38025	470	AT2G38025.1	similar to OTU-like cysteine protease family protein [Arabidopsis thaliana] (TAIR:AT3G57810.1); similar to OTU-like cysteine protease family protein [Arabidopsis thaliana] (TAIR:AT3G57810.3); similar to OTU-like cysteine protease family protein [Arab	234	ENV	Ch/E/IM	9.47	26.27	100.0	0.0	0.0	3.0	chaperone and protease	35.2 not assigned. unknown	chloroplast	Y	C	-	
AT2G38040	471	AT2G38040.1	CAC3 (acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit); acetyl-CoA carboxylase	769	ENV	Ch/E & Ch/S	5.61	85.3	95.458873444071 3	2.0357002741584 9	2.5054262817701 6	514.0	metabolism lipid	11.1.1 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	chloroplast	Y	C	envelope-inner-peripheral-stromal-side	

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AT2G38140	472	AT2G38140.1	PSRP4 (PLASTID-SPECIFIC RIBOSOMAL PROTEIN 4); structural constituent of ribosome	118	STR-ENV	Ch/E ?	10.17	12.78	26.212628759875	73.787371240125	0.0	11.0	translation stroma	29.2.1.1.1.1.31 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S31	chloroplast	Y	C	plastid ribosome	
AT2G38270	473	AT2G38270.1	CXIP2 (CAX-INTERACTING PROTEIN 2); electron carrier/ protein disulfide oxidoreductase	293	STR		7.72	32.2	0.0	100.0	0.0	16.0		34.21 transport.calcium	chloroplast	Y	C	plastid stroma	
AT2G38530	474	AT2G38530.1	LTP2 (LIPID TRANSFER PROTEIN 2); lipid binding	118			9.32	11.93				3.0		11.6 lipid metabolism.lipid transfer proteins etc	secreted		S	-	
AT2G38540	475	AT2G38540.1	LP1 (nonspecific lipid transfer protein 1)	118	THY		9.3	11.75	0.0	0.0	100.0	22.0		11.6 lipid metabolism.lipid transfer proteins etc	secreted		S	-	

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AT2G38550	476	AT2G38550.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57280.1); similar to non-green plastid inner envelope membrane protein precursor (GB:AAA84891.1); contains InterPro domain Protein of unknown function UPF0136 , Transmembrane; (InterPro: IPR00	335	ENV	Ch/E/IM	6.99	36.7	100.0	0.0	0.0	52.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	envelope-inner-integral	4.0
AT2G38810	477	AT2G38810.1	HTA8; DNA binding	136	THY-ENV	other	10.47	14.37	30.888133963744 9	9.6609675714206 2	59.450898464834 5	7.0	DNA binding	28.1.3 DNA.synthesis/chromatin structure. histone	undefined	Y	C	-	
AT2G39080	478	AT2G39080.1	binding / catalytic	351	STR		7.65	38.25	0.0	100.0	0.0	29.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	

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AT2G39290	479	AT2G39290.1	PGP1/PGPS1/PGS1 (PHOSPHATIDYLGLYCEROLPHOSPHATE SYNTHASE 1); CDP-alcohol phosphatidyltransferase/ CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	296	ENV	Ch/E & other	10.3	32.15	100.0	0.0	0.0	13.0	metabolism lipid	11.10 lipid metabolism.glycolipid synthesis; 11.3 lipid metabolism.Phospholipid synthesis	undefined	Y	C	plastid; mitochondria	2.0
AT2G39470	480	AT2G39470.1	PPL2 (PSBP-LIKE PROTEIN 2); calcium ion binding	238		Lum	8.89	26.96	0.0	0.0	100.0	7.0		1.1.6 PS.lightreaction.NADH DH	undefined		C	thylakoid-peripheral-lumenal-side	
AT2G39730	481	AT2G39730.1	RCA (RUBISCO ACTIVASE)	446	STR	Ch & other	7.54	49.1	14.514142717456 9	77.087493896688 1	8.3983633858550 4	3757.0	chaperone and protease	1.3.13 PS.calvincycle.rubisco interacting	chloroplast	Y	C	plastid stroma	
AT2G39730	482	AT2G39730.2	RCA (RUBISCO ACTIVASE)	446	STR	Ch & other	7.54	49.1	14.514142717456 9	77.087493896688 1	8.3983633858550 4	3757.0	chaperone and protease	1.3.13 PS.calvincycle.rubisco interacting	chloroplast	Y	C	plastid stroma	
AT2G39930	483	AT2G39930.1	ATISA1/ISA1 (ISOAMYLASE 1); alpha-amylase/ isoamylase	783			5.77	89.48	0.0	100.0	0.0	4.0		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	undefined	Y	C	plastid	

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AT2G40010	484	AT2G40010.1	60S acidic ribosomal protein P0 (RPP0A)	317	ENV	Ch/E & other	5.18	33.66	100.0	0.0	0.0	3.0	translation cytosol	29.2.1.2.2.80 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P0	secreted		S	cytosol	
AT2G40030	485	AT2G40030.1	NRPD1b (nuclear RNA polymerase D 1b); DNA binding / DNA-directed RNA polymerase	501			5.88	218.22	0.0	0.0	100.0	1.0		27.2 RNA.transcription	undefined			-	
AT2G40100	486	AT2G40100.1	LHCB4.3 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding	276	THY	Ch/Th	5.22	30.21	1.9967944030032 7	0.0	98.003205596996 7	92.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	undefined	Y	C	thylakoid-integral	3.0
AT2G40300	487	AT2G40300.1	ATFER4 (FERRITIN 4); ferric iron binding	259	STR		6.15	29.02	0.0	100.0	0.0	20.0		15.2 metal handling. binding, chelation and storage	chloroplast	Y	C	plastid stroma	
AT2G40490	488	AT2G40490.1	HEME2; uroporphyrinogen decarboxylase	394	STR	Ch/E & Ch/S	8.28	43.58	2.3135120993913 7	97.686487900608 6	0.0	175.0	metabolism vitamin and pigment	19.7 tetrapyrrole synthesis.uroporphyrinogen decarboxylase	chloroplast	Y	C	plastid stroma	

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AT2G40510	489	AT2G40510.1	40S ribosomal protein S26 (RPS26A)	133	ENV	Ch & other	11.09	14.84	100.0	0.0	0.0	3.0	translation cytosol	29.2.1.2.1.26 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S26	undefined			-	
AT2G40690	490	AT2G40690.1	GLY1 (SUPPRESSOR OF FATTY ACID DESATURASE DEFICIENCY 1); glycerol-3-phosphate dehydrogenase (NAD+)	300	ENV	Ch/E ?	8.75	45.09	100.0	0.0	0.0	10.0	metabolism lipid ?	11.5.2 lipid metabolism.glycerol metabolism.Glycerol-3-phosphate dehydrogenase (NAD+)	undefined			-	
AT2G41680	491	AT2G41680.1	thioredoxin reductase, putative / NADPH-dependent thioredoxin reductase, putative	529	STR		6.3	57.95	0.0	100.0	0.0	41.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	

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AT2G41950	492	AT2G41950.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO23423.1); contains domain S-adenosyl-L-methionine-dependent methyltransferases (SSF53335)	266	STR		5.54	30.02	0.0	100.0	0.0	10.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT2G42130	493	AT2G42130.4	Identical to Probable plastid-lipid-associated protein 13, chloroplast precursor (PAP13) [Arabidopsis Thaliana] (GB:Q8S9M1;GB:O48521;GB:Q84X37;GB:Q84X38;GB:Q84X39;GB:Q8GY49); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G58010.1); simi	299	THY-STR		4.84	27.66	0.0	31.707757666861 3	68.292242333138 7	35.0		26.31* misc.fibrillins	chloroplast	Y		thylakoid-peripheral-stromal-side	

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AT2G42220	494	AT2G42220.1	rhodanese-like domain-containing protein	234	THY	Ch/Th	8.86	25.51	12.168874940808 4	0.0	87.831125059191 6	22.0	chaperone and protease	26.23 misc.rhodanese	chloroplast	Y	C	thylakoid	1.0
AT2G42530	495	AT2G42530.1	COR15B	141	STR		6.62	14.96	0.0	100.0	0.0	26.0		20.2.2 stress.abiotic.cold	undefined	Y	C	plastid stroma	
AT2G42540	496	AT2G42540.1	COR15A (COLD-REGULATED 15A)	127	STR		6.61	13.45	0.0	100.0	0.0	29.0		20.2.2 stress.abiotic.cold	undefined	Y	M	plastid stroma	
AT2G42740	497	AT2G42740.1	RPL16A (ribosomal protein large subunit 16A); structural constituent of ribosome	182	ENV	Ch/E & other	9.93	20.83	100.0	0.0	0.0	2.0	translation cytosol	29.2.1.2.2.11 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L11	undefined			-	
AT2G42770	498	AT2G42770.1	peroxisomal membrane 22 kDa family protein	232	ENV	Ch/E/IM	9.81	25.91	100.0	0.0	0.0	18.0	transporter ?	35.1 not assigned.no ontology	undefined	Y		envelope	2.0
AT2G43030	499	AT2G43030.1	ribosomal protein L3 family protein	271	STR-ENV	Ch/S	10.43	29.36	20.754501169337 5	77.248172376505 7	1.997326454156 85	211.0	translation stroma	29.2.1.1.1.2.3 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L3	chloroplast	Y	C	plastid ribosome	
AT2G43090	500	AT2G43090.1	aconitase C-terminal domain-containing protein	251	STR		6.33	26.79	0.0	100.0	0.0	17.0		13.1.4.4 amino acid metabolism.synthesis.branched chain group.leucine specific	chloroplast	Y	C	-	

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AT2G43240	501	AT2G43240.1	nucleotide-sugar transmembrane transporter	406	ENV	Ch/E ?	8.92	86.95	100.0	0.0	0.0	6.0	unknown	34.2 transport. sugars	undefined			-	8.0
AT2G43560	502	AT2G43560.1	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	223	THY-STR	Ch/Th/Lum	8.4	23.56	22.219258403167 8	24.323527378213 2	53.457214218618 9	18.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT2G43630	503	AT2G43630.1	similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:AT3G59640.2); similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:AT3G59640.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46269.1)	274	ENV	Ch/E & Ch/Th	8.29	30.7	100.0	0.0	0.0	8.0	RNA binding ?	35.2 not assigned. unknown	chloroplast	Y	C	plastid	1.0

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AT2G43710	504	AT2G43710.1	SSI2 (fatty acid biosynthesis 2); acyl-[acyl-carrier-protein] desaturase	401	THY-STR		6.05	45.69	0.0	19.5983105649505	80.401689435049 5	11.0		11.1.15 lipid metabolism.FA synthesis and FA elongation.ACP desaturase	chloroplast	Y	C	plastid stroma	
AT2G43750	505	AT2G43750.1	OASB (O-ACETYL SERINE (THIOL) LYASE B); cysteine synthase	392	STR	Ch/S & other	8.13	41.65	6.3673467391801 2	92.4071195820107	1.2255336788091 8	334.0	metabolism aa Cys	13.1.5.3.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	chloroplast	Y	C	plastid stroma	
AT2G43945	506	AT2G43945.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G59870.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN60471.1); contains InterPro domain Gamma thionin; (InterPro:IPR008176)	289	STR		6.25	32.16	0.0	100.0	0.0	21.0		34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	plastid stroma	

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AT2G43950	507	AT2G43950.1	OEP37; ion channel	343	ENV	Ch/E/OM	9.16	38.83	95.618147202831 2	0.0	4.3818527971687 8	46.0	transporter ion channel	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-outer	
AT2G44040	508	AT2G44040.1	dihydrodipicolinate reductase family protein	347	STR		6.01	37.55	0.0	100.0	0.0	39.0		13.1.3.5.2 amino acid metabolism.synthesis.aspartate family.lysine.dihydrodipicolinate reductase	undefined	Y	C	plastid stroma	
AT2G44050	509	AT2G44050.1	COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase	227	STR		8.62	24.02	0.0	100.0	0.0	15.0		18.3.2 Co-factor and vitamine metabolism.riboflavin.riboflavin synthase	chloroplast	Y	C	plastid	
AT2G44530	510	AT2G44530.1	ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative	394			6.71	42.62	0.0	100.0	0.0	3.0		23.1.3 nucleotide metabolism.synthesis.PRS-PP	chloroplast	Y	C	plastid stroma	
AT2G44610	511	AT2G44610.1	RAB6; GTP binding	208	ENV	Ch/E ?	7.67	23.13	100.0	0.0	0.0	3.0	signalling / SNARE effector	30.5 signalling.G-proteins	undefined			-	

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AT3G08740	569	AT3G08740.1	elongation factor P (EF-P) family protein	236	STR		8.61	26.22	0.0	100.0	0.0	55.0		29.2.4 protein.synthesis.elongation	chloroplast	Y	C	plastid stroma	
AT2G44640	512	AT2G44640.1	similar to PDE320 (PIGMENT DEFECTIVE 320) [Arabidopsis thaliana] (TAIR:AT3G06960.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70456.1)	451	ENV	Ch/E	8.8	49.83	90.712942091249 7	0.0	9.2870579087503 3	55.0	unknown	35.2 not assigned.unknown	undefined		C	envelope	
AT2G44650	513	AT2G44650.1	CHL-CPN10 (chloroplast chaperonin 10)	139	ENV-STR	Ch/S	8.74	15.05	54.523820970145 7	45.476179029854 3	0.0	29.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT2G44870	514	AT2G44870.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO62235.1); contains domain Zinc beta-ribbon (SSF57783)	248	ENV	Ch/E/IM	9.93	28.07	100.0	0.0	0.0	9.0	RNA transcription ?	35.2 not assigned.unknown	undefined	Y	M	-	2.0

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AT2G44920	515	AT2G44920.2	thylakoid lumenal 15 kDa protein, chloroplast	224	THY	Lum	7.55	23.77	0.0	0.0	100.0	18.0		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT2G45290	516	AT2G45290.1	transketolase, putative	741	STR	Ch/S	6.12	79.92	11.781837913427 8	86.598398027332 6	1.619764 0592396 1	497.0	metabolism carbon	1.3.8 PS.calvin cyle.transketolase	chloroplast	Y	C	-	
AT2G45300	517	AT2G45300.1	3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase	520	STR		6.29	55.73	0.0	100.0	0.0	31.0		13.1.6.1.6 amino acid metabolism.synthesis.aromatic aa.chorismate.5-enolpyruvylshikimate-3-phosphate synthase	chloroplast	Y	C	-	
AT2G45440	518	AT2G45440.1	DHDPS2 (DIHYDRODIPICOLINATE SYNTHASE); dihydrodipicolinate synthase	365			7.17	40.29	0.0	100.0	0.0	8.0		13.1.3.5.1 amino acid metabolism.synthesis.aspartate family.lysine.dihydrodipicolinate synthase	undefined	Y	C	-	
AT2G45540	519	AT2G45540.1	WD-40 repeat family protein / beige-related	2946			5.56	321.93	0.0	24.528678553158 6	75.47132 1446841 4	4.0		35.1 not assigned. no ontology	other (e.g. cytoplasm)			-	2.0
AT2G45740	520	AT2G45740.1	PEX11D	236	ENV	Ch/E ?	9.98	25.94	100.0	0.0	0.0	1.0	unknown	35.1 not assigned. no ontology	undefined		S	peroxisome	2.0

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AT2G45770	521	AT2G45770.1	CPFTSY (ferric reductase deficient 4); GTP binding	366	Mix	Ch	7.59	39.67	34.474715888551 7	32.348258327048 8	33.177025784399 5	10.0	protein targeting	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT2G45990	522	AT2G45990.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO39632.1); contains domain HAD-like (SSF56784)	268	STR		5.05	30.11	0.0	100.0	0.0	32.0		35.2 not assigned. unknown	undefined			plastid stroma	
AT2G46100	523	AT2G46100.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39659.1); contains domain SSF54427 (SSF54427)	240	ENV	Ch/E/IM	8.86	26.84	100.0	0.0	0.0	7.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	

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AT2G46820	524	AT2G46820.1	PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA); DNA binding	174	THY	Ch/Th	7.72	18.48	7.4015647236884 7	0.0	92.598435276311 5	55.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid	2.0
AT2G46910	525	AT2G46910.1	plastid-lipid associated protein PAP / fibrillin family protein	284			8.34	31.58	0.0	100.0	0.0	4.0		26.31* misc.fibrillins	chloroplast	Y	C	plastoglobules	
AT2G47220	526	AT2G47220.1	3' exoribonuclease family domain 1 protein-related	469	STR		5.42	52.4	0.0	100.0	0.0	10.0		27.1.19 RNA.processing.ribonucleases	undefined			-	
AT2G47390	527	AT2G47390.1	serine-type endopeptidase/ serine-type peptidase	961	STR		5.99	106.26	0.0	100.0	0.0	42.0		29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma	
AT2G47400	528	AT2G47400.1	CP12-1 (CP12 domain-containing protein 1)	124	STR-ENV	Ch/E ?	4.85	13.48	26.212628759875	73.787371240125	0.0	14.0	metabolism carbon	1.3.14* PS.calvin cycle regulation CP12	undefined	Y	C	-	
AT2G47450	529	AT2G47450.1	CAO (CHAOS); chromatin binding	373			4.52	41.27	0.0	100.0	0.0	7.0		29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	plastid stroma	

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AT2G47730	530	AT2G47730.1	ATGSTF8 (GLUTATHIONE S-TRANSFERASE 8); glutathione transferase	263	STR		8.49	29.23	0.0	100.0	0.0	28.0		26.9 misc.glutathione S transferases	chloroplast	Y	C	-	
AT2G47840	531	AT2G47840.1	tic20 protein-related	208	ENV	Ch/E/IM	10.28	22.91	94.787457828387 5	0.0	5.2125421716124 6	37.0	protein targeting Tic ?	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope-inner-integral	4.0
AT2G47910	532	AT2G47910.1	CRR6 (CHLORORESPIRATORY REDUCTION 6)	246			5.34	28.02	0.0	100.0	0.0	5.0		1.1.6.1* PS.lightreaction.NADH DH.assembly	undefined		M	plastid stroma	
AT2G47940	533	AT2G47940.1	DEGP2 (DEGP PROTEASE 2); serine-type peptidase/ trypsin	607	STR-ENV	Ch/E & Ch/S	5.7	66.8	24.226403607846 9	75.773596392153 1	0.0	50.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma	
AT3G01120	534	AT3G01120.1	MTO1 (METHIONINE OVERACCUMULATION 1)	563	STR		6.4	59.91	0.0	100.0	0.0	10.0		13.1.3.4.1 amino acid metabolism.synthesis.aspartate family.methionine.cystathionine gamma-synthase	chloroplast	Y	C	-	1.0
AT3G01390	535	AT3G01390.1	VMA10 (VACUOLAR MEMBRANE ATPASE 10)	110	ENV	other	5.76	12.39	100.0	0.0	0.0	3.0	transporter ATPase	34.1 transport.p- and v-ATPases	undefined			-	

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AT3G01440	536	AT3G01440.1	oxygen evolving enhancer 3 (PsbQ) family protein	220	THY	Ch/Th	7.67	24.78	8.6311509957500 6	0.0	91.368849004249 9	18.0	PS PSII OEE	1.1.6 PS.lightreaction.NADH DH	undefined	Y	C	thylakoid-peripheral-lumenal-side	
AT3G01480	537	AT3G01480.1	CYP38 (CYCLOPHILIN 38); peptidyl-prolyl cis-trans isomerase	437	THY	Ch/E & Ch/Th/Lum	5.05	47.98	6.1028781501227 6	2.8632212601385 2	91.033900589738 7	77.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT3G01500	538	AT3G01500.1	CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	270	ENV-STR	Ch	5.53	29.5	58.784535223781 4	40.851659117421 4	0.36380565879719 3	1330.0	metabolism carbon	8.3 TCA / org.transformation.carbonic anhydrases	chloroplast			plastid stroma	
AT3G01500	539	AT3G01500.3	CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	270	ENV-STR	Ch	5.53	29.5	58.784535223781 4	40.851659117421 4	0.36380565879719 3	1330.0	metabolism carbon	8.3 TCA / org.transformation.carbonic anhydrases	chloroplast			plastid stroma	
AT3G02360	540	AT3G02360.1	6-phosphogluconate dehydrogenase family protein	486	STR		7.02	53.57	0.0	100.0	0.0	36.0		7.1.3 OPP.oxidative PP.6-phosphogluconate dehydrogenase	secreted		S	-	
AT3G02450	541	AT3G02450.1	cell division protein ftsH, putative	622	ENV	Ch/E/IM	9.67	69.41	87.913653438274 6	0.0	12.086346561725 4	10.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	-	3.0

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AT3G02660	542	AT3G02660.1	EMB2768 (EMBRYO DEFECTIVE 2768); ATP binding / aminoacyl-tRNA ligase	511	STR		6.01	56.61	0.0	100.0	0.0	15.0		29.1.1 protein.aa activation.tyrosine-tRNA ligase	chloroplast	Y	C	mitochondria; plastid stroma	
AT3G02730	543	AT3G02730.1	ATF1/TRXF1 (THIOREDOXIN F-TYPE 1); thiol-disulfide exchange intermediate	178	THY-STR		9.12	19.32	0.0	45.525796433193 8	54.474203566806 2	25.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT3G02780	544	AT3G02780.1	IDI2/IPIAT1/IPP2 (ISOPENTENYL DIPHOSPHATE ISOMERASE 2, ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE 2); isopentenyl-diphosphate delta-isomerase	284	Mix	Ch/E ?	6.09	32.6	14.920853107486 7	42.001530542667 4	43.077616349845 9	13.0	metabolism vitamin and pigment	16.1.2.7 secondary metabolism.isoprenoids.mevalonate pathway.isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase	chloroplast	Y	C	cytosol; mitochondria	

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AT3G02900	545	AT3G02900.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16660.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62132.1)	162	ENV	Ch/E/IM	9.51	17.32	93.345772566040 2	0.0	6.6542274339598 1	29.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	1.0
AT3G03710	546	AT3G03710.1	RIF10 (RESISTANT TO INHIBITION WITH FSM 10); 3'-5'-exoribonuclease/ RNA binding / nucleic acid binding	922	STR		5.4	99.56	0.0	100.0	0.0	63.0		27.1.19 RNA.processing.ribonucleases	chloroplast	Y	C	plastid stroma	
AT3G04260	547	AT3G04260.1	PTAC3 (PLASTID TRANSCRIPTIONALLY ACTIVE3); DNA binding	913			4.94	103.12	0.0	100.0	0.0	2.0		28.3* DNA.plastid nucleoid interacting	chloroplast	Y	C	plastid	
AT3G04340	548	AT3G04340.1	EMB2458 (EMBRYO DEFECTIVE 2458); ATPase	960	ENV	Ch/E/IM	8.01	111.01	100.0	0.0	0.0	36.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast			plastid	

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AT3G04550	549	AT3G04550.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28500.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65032.1)	449	STR		5.77	50.2	0.0	96.059190325445 2	3.9408096745548 4	87.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT3G04790	550	AT3G04790.1	ribose 5-phosphate isomerase-related	276	STR	Ch	5.72	29.3	4.2897972402739 4	95.710202759726 1	0.0	319.0	metabolism carbon	1.3.10 PS.calvincyle.Rib5P Isomerase	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT3G04840	551	AT3G04840.1	40S ribosomal protein S3A (RPS3aA)	262	ENV	Ch/E & other	9.77	29.85	100.0	0.0	0.0	2.0	translation cytosol	29.2.1.2.1.53 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S3A	other (e.g. cytoplasm)			cytosol	
AT3G04870	552	AT3G04870.1	ZDS (ZETA-CAROTENE DESATURASE); carotene 7,8-desaturase	558	ENV	Ch/E & PG	7.03	61.63	90.292178334441 2	9.7078216655587 8	0.0	43.0	metabolism vitamin and pigment	16.1.4.3 secondary metabolism.isoprenoids.carotenoids.zeta-carotene desaturase	undefined	Y	C	plastid	

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AT3G04890	553	AT3G04890.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G46100.1); similar to unknown [Picea sitchensis] (GB:ABK21558.1); contains domain SSF54427 (SSF54427)	216	ENV	Ch/E/IM	6.61	24.43	100.0	0.0	0.0	4.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	
AT3G04940	554	AT3G04940.1	ATCYSD1 (Arabidopsis thaliana cysteine synthase D1); cysteine synthase	324			5.23	34.29	0.0	49.367597204202 1	50.632402795797 9	5.0		13.1.5.3.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	other (e.g. cytoplasm)			-	
AT3G05350	555	AT3G05350.1	aminopeptidase	548	STR		5.32	60.85	0.0	100.0	0.0	18.0		29.5 protein.degradation	undefined			plastid stroma	
AT3G05625	556	AT3G05625.1	binding	257			6.95	28.95	0.0	100.0	0.0	8.0		26.33* misc.tetratricopeptide repeat (TPR) unknown function	chloroplast	Y	C	plastid	

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AT3G06030	557	AT3G06030.1	ANP3 (Arabidopsis NPK1-related protein kinase 3); kinase	651			8.41	71.65	0.0	100.0	0.0	1.0		29.4 protein.postranslational modification	undefined	Y		-	
AT3G06350	558	AT3G06350.1	EMB3004/MEE32 (EMBRYO DEFECTIVE 3004); 3-dehydroquinate dehydratase/ NADP binding / binding / catalytic/ shikimate 5-dehydrogenase	603	STR		6.4	65.79	0.0	100.0	0.0	14.0		13.1.6.1.10 amino acid metabolism.synthesis.aromatic aa.chorismate.dehydroquinate/shikimate dehydrogenase	chloroplast	Y	C	plastid	
AT3G06510	559	AT3G06510.1	SFR2 (SENSITIVE TO FREEZING 2); hydrolase, hydrolyzing O-glycosyl compounds	622	ENV	Ch/E/OM	8.79	70.77	100.0	0.0	0.0	126.0	stress freezing	26.3 misc.gluco-, galacto- and mannosidases	secreted		S	envelope -outer	1.0
AT3G06730	560	AT3G06730.1	thioredoxin family protein	183			5.64	20.67	0.0	100.0	0.0	4.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid	
AT3G06960	561	AT3G06960.1	PDE320 (PIGMENT DEFECTIVE 320)	479	ENV	Ch/E ?	6.36	52.82	100.0	0.0	0.0	13.0	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	

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AT3G07430	562	AT3G07430.1	EMB1990 (EMBRYO DEFECTIVE 1990)	232	ENV	Ch/E/IM	10.66	24.92	100.0	0.0	0.0	8.0	cytochrome biogenesis ?	33.99 development.unspecified	undefined	Y	C	-	
AT3G07440	563	AT3G07440.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G48530.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN82702.1)	235			9.35	28.54				1.0		35.2 not assigned. unknown	undefined		M	-	
AT3G07630	564	AT3G07630.1	ADT2 (AROGENATE DEHYDRATASE 2); arogenate dehydratase/ prephenate dehydratase	381			7.67	42.11	0.0	100.0	0.0	6.0		13.1.6.3.1 amino acid metabolism.synthesis.aromatic aa.phenylalanine.arogenate dehydratase / prephenate dehydratase	undefined	Y	C	plastid stroma	
AT3G07770	565	AT3G07770.1	ATP binding	799	STR		5.25	90.95	0.0	100.0	0.0	40.0		20.2.1 stress.abiotic.heat	mitochondrion	Y	M	-	
AT3G08010	566	AT3G08010.1	ATAB2; RNA binding	374			5.0	41.91	0.0	100.0	0.0	4.0		27.4 RNA.RNA binding	chloroplast	Y	C	plastid	

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AT3G08580	567	AT3G08580.1	AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter / binding	381			9.83	41.47	0.0	0.0	100.0	6.0		34.9 transport.metabolite transporters at the mitochondrial membrane	undefined	Y		mitochondria	3.0
AT3G08640	568	AT3G08640.1	alphavirus core protein family	337	ENV	Ch/E/IM	9.0	35.25	100.0	0.0	0.0	29.0	unknown	35.1 not assigned.no ontology	chloroplast	Y	C	-	3.0
AT3G08920	570	AT3G08920.1	rhodanese-like domain-containing protein	214	THY-ENV	Ch/E ?	9.32	23.78	44.696379155785 9	0.0	55.303620844214 1	22.0	unknown	26.23 misc.rhodanese	undefined		M	thylakoid	1.0
AT3G08940	571	AT3G08940.2	LHCB4.2 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding	287	THY	Ch/Th	5.85	31.19	2.7437205356621 6	0.0	97.256279464337 8	380.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	
AT3G09440	572	AT3G09440.1	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	649	ENV-STR	Ch/E & other	4.97	71.14	72.472608297152 8	26.043463843078 8	1.483927859768 4 5	106.0	chaperone and protease	20.2.1 stress.abiotic.heat	other (e.g. cytoplasm)			-	
AT3G09580	573	AT3G09580.1	amine oxidase family protein	477	ENV	Ch/E/IM	7.02	52.25	96.144762448164 5	0.0	3.855237551835 5 1	25.0	metabolism vitamin and pigment ?	16.1.4 secondary metabolism.isoprenoids.carotenoids	undefined	Y	C	plastid	

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AT3G10050	574	AT3G10050.1	OMR1 (L-O-METHYL THREONINE RESISTANT 1); L-threonine ammonia-lyase	592			7.2	64.63	0.0	100.0	0.0	2.0		13.1.4.5.1 amino acid metabolism.synthesis.branched chain group.isoleucine specific.threonine ammonia-lyase	chloroplast	Y	C	-	1.0
AT3G10060	575	AT3G10060.1	immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative	230	THY	Lum	9.66	24.5	0.0	0.0	100.0	21.0		29.6 protein.folding	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT3G10230	576	AT3G10230.1	LYC (LYCOPENE CYCLASE); lycopene beta cyclase	501	ENV	Ch/E ?	7.6	56.17	100.0	0.0	0.0	3.0	metabolism vitamin and pigment	16.1.4.5 secondary metabolism.isoprenoids.carotenoids.lycopene beta cyclase	undefined			-	
AT3G10350	577	AT3G10350.1	anion-transporting ATPase family protein	411			7.63	44.75	0.0	100.0	0.0	9.0		34.18.1 transport.unspecified anions.arsenite-transporting ATPase	chloroplast	Y	C	plastid	
AT3G10670	578	AT3G10670.1	ATNAP7 (Arabidopsis thaliana non-intrinsic ABC protein 7)	338	STR		6.61	36.93	0.0	100.0	0.0	49.0		14 S-assimilation	chloroplast	Y	C	plastid stroma	

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AT3G10680	579	AT3G10680.1	heat shock protein-related	490	ENV	Ch/E/IM	8.95	54.19	100.0	0.0	0.0	4.0	chaperone and protease	20.2.1 stress.abiotic.heat	undefined	Y	C	-	1.0
AT3G10690	580	AT3G10690.1	DNA gyrase subunit A family protein	950			6.46	104.53	0.0	0.0	100.0	2.0		28.2 DNA.repair	chloroplast	Y	C	plastid	
AT3G10840	581	AT3G10840.1	hydrolase, alpha/beta fold family protein	466	ENV	Ch/E/IM	8.59	50.88	100.0	0.0	0.0	31.0	metabolism lipid	11.9.2 lipid metabolism.lipid degradation.lipases	chloroplast	Y	C	-	
AT3G10920	582	AT3G10920.1	MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); manganese superoxide dismutase	231			8.46	25.44	0.0	100.0	0.0	2.0		21.6 redox.dismutases and catalases	undefined		M	mitochondria	
AT3G11170	583	AT3G11170.1	FAD7 (FATTY ACID DESATURASE 7); omega-3 fatty acid desaturase	446	ENV	Ch/E/IM	8.14	51.17	100.0	0.0	0.0	45.0	metabolism lipid	11.2.3 lipid metabolism.FA desaturation.omega 3 desaturase	chloroplast	Y	C	envelope-inner-integral	4.0
AT3G11510	584	AT3G11510.1	40S ribosomal protein S14 (RPS14B)	150	ENV	Ch/E & other	10.6	16.27	86.476285785767 9	13.523714214232 1	0.0	10.0	translation cytosol	29.2.1.2.1.14 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S14	other (e.g. cytoplasm)			cytosol	

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AT3G11560	585	AT3G11560.2	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06220.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15863.1)	619	ENV	Ch/E/IM	8.32	69.68	100.0	0.0	0.0	19.0	transporter K+/H+?	35.2 not assigned. unknown	undefined	Y	C	-	2.0
AT3G11630	586	AT3G11630.1	2-cys peroxiredoxin, chloroplast (BAS1)	266	STR	Ch	6.91	29.09	13.661924772101 5	85.461564198977 5	0.876511028921062	486.0	redox	21.5 redox.peri redoxins	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT3G11940	587	AT3G11940.1	ATRPS5A (RIBOSOMAL PROTEIN 5A); structural constituent of ribosome	207	STR	Ch & other	9.65	22.92	0.0	100.0	0.0	2.0	translation cytosol	29.2.1.2.1.5 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S5	undefined			-	
AT3G11950	588	AT3G11950.1	homogentisate farnesyltransferase/ homogentisate geranylgeranyltransferase/ homogentisate solanesyltransferase/ prenyltransferase	572	ENV	Ch/E/IM	5.15	106.65	94.212780275916 9	0.0	5.787219724083 8	50.0	metabolism isoprenoids	16.1 secondary metabolism.isoprenoids	other (e.g. cytoplasm)			-	7.0

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AT3G12080	589	AT3G12080.1	EMB2738 (EMBRYO DEFECTIVE 2738); GTP binding	663			6.14	73.12	0.0	100.0	0.0	3.0		29.2.7* protein.synthesis.ribosome biogenesis	chloroplast	Y	C	plastid	
AT3G12110	590	AT3G12110.1	ACT11 (ACTIN-11); structural constituent of cytoskeleton	377	ENV-STR	Ch/E & other	5.22	41.67	56.118865710137 3	43.881134289862 7	0.0	22.0	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT3G12780	591	AT3G12780.1	PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase	481	STR	Ch/S & other	5.91	50.11	7.4384641418664 1	89.785803749249 1	2.7757321088844 8	2675.0	metabolism carbon	1.3.3 PS.calvincyle.phosphoglycerate kinase	chloroplast	Y	C	plastid stroma	
AT3G13070	592	AT3G13070.1	CBS domain-containing protein / transporter associated domain-containing protein	661	ENV	Ch/E/IM	5.0	73.75	100.0	0.0	0.0	31.0	transporter Mg & Co ?	35.1 not assigned. no ontology	chloroplast	Y	C	-	5.0
AT3G13120	593	AT3G13120.1	30S ribosomal protein S10, chloroplast, putative	191	STR		8.99	20.83	0.0	100.0	0.0	21.0		29.2.1.1.1.1.10 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S10	chloroplast	Y	C	plastid ribosome	

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AT3G13180	594	AT3G13180.1	NOL1/NOP2/sun family protein / antitermination NusB domain-containing protein	523			9.11	58.34	0.0	100.0	0.0	3.0		35.1 not assigned. no ontology	chloroplast	Y	C	-	
AT3G13470	595	AT3G13470.1	chaperonin, putative	596	STR-ENV	Ch & other	5.59	63.34	15.873331593834 7	82.134168718509 8	1.992499 6876555 6	1248.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT3G13490	596	AT3G13490.1	OVA5 (OVULE ABORTION 5); ATP binding / aminoacyl-tRNA ligase	602			5.73	67.58	0.0	100.0	0.0	7.0		29.1.6 protein.aa activation.lysine-tRNA ligase	undefined	Y	M	mitochondria; plastid stroma	
AT3G13800	597	AT3G13800.1	metallo-beta-lactamase family protein	361			7.21	40.38	0.0	100.0	0.0	1.0		35.1 not assigned. no ontology	chloroplast	Y	C	-	
AT3G14110	598	AT3G14110.1	FLU (FLUORESCENT IN BLUE LIGHT); binding	316	THY	Ch/E & Ch/Th	9.09	34.58	12.925729163927 1	0.0	87.074270836072 9	13.0	metabolism vitamin and pigment	19.40 tetrapyrrole synthesis.regulation	chloroplast		C	envelope-inner; thylakoid	1.0
AT3G14270	599	AT3G14270.1	phosphatidylinositol-4-phosphate 5-kinase family protein	1791			5.62	200.83	0.0	100.0	0.0	1.0		30.4.1 signalling.phosphinositides. phosphatidylinositol-4-phosphate 5-kinase	undefined			-	

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AT3G14390	600	AT3G14390.1	diaminopimelate decarboxylase, putative / DAP carboxylase, putative	484	STR		6.51	53.55	0.0	100.0	0.0	54.0		13.1.3.5.5 amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate decarboxylase	chloroplast	Y	C	-	
AT3G14415	601	AT3G14415.1	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	367	STR	other	8.99	40.3	10.566248436418 8	81.298938839898 1	8.1348127236831 1	156.0	stress oxidative	1.2.2 PS.photorespiration.glycolate oxydase	other (e.g. cytoplasm)			peroxisome	
AT3G14420	602	AT3G14420.1	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	367	STR	other	9.15	40.34	12.370468274257 1	75.724710052175 1	11.904821673567 8	181.0	stress oxidative	1.2.2 PS.photorespiration.glycolate oxydase	other (e.g. cytoplasm)			peroxisome	

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AT3G14930	603	AT3G14930.1	HEME1; uroporphyrinogen decarboxylase	418	STR		6.64	46.25	0.0	100.0	0.0	49.0		19.7 tetrapyrrole synthesis.uroporphyrinogen decarboxylase	undefined	Y	C	plastid stroma	
AT3G15110	604	AT3G15110.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO39343.1)	266			6.18	28.61	0.0	0.0	100.0	4.0		35.2 not assigned. unknown	undefined		M	-	3.0
AT3G15190	605	AT3G15190.1	chloroplast 30S ribosomal protein S20, putative	202	STR-ENV	Ch/S	10.14	21.82	46.864719070654 8	53.135280929345 2	0.0	43.0	translation stroma	29.2.1.1.1.1.20 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S20	chloroplast	Y	C	plastid ribosome	
AT3G15356	606	AT3G15356.1	legume lectin family protein	271			8.9	29.75				2.0		26.16 misc.myrosinases-lectin-jacalin	secreted		S	-	
AT3G15360	607	AT3G15360.1	ATHM4 (Arabidopsis thioredoxin M-type 4); thiol-disulfide exchange intermediate	193	STR-ENV	Ch & other	9.61	21.17	15.789896207797 3	74.079746318770 1	10.130357473432 6	77.0	redox	21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	

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AT3G15520	608	AT3G15520.1	peptidyl-prolyl cis-trans isomerase TLP38, chloroplast / thylakoid lumen PPIase of 38 kDa / cyclophilin / rotamase	466	THY	Lum	6.56	50.48	0.0	0.0	100.0	35.0		29.6 protein.folding	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT3G15840	609	AT3G15840.1	PIFI (POST-ILLUMINATION CHLOROPHYLL FLUORESCENCE INCREASE)	268			5.83	29.69	0.0	100.0	0.0	3.0		1.1.40 PS.lightreaction.cyclic electron flow-chlororespiration	chloroplast	Y	C	plastid	
AT3G15850	610	AT3G15850.1	FAD5 (FATTY ACID DESATURASE 5); oxidoreductase	371	ENV	Ch/E/IM	9.27	42.58	100.0	0.0	0.0	4.0	metabolism lipid	11.2.1 lipid metabolism.FA desaturation.desaturase	chloroplast	Y	C	-	3.0
AT3G15900	611	AT3G15900.1	similar to unknown [Populus trichocarpa] (GB:ABK95820.1)	141			10.16	15.01	0.0	0.0	100.0	3.0		35.2 not assigned.unknown	chloroplast	Y	C	-	2.0
AT3G16000	612	AT3G16000.1	MFP1 (MAR BINDING FILAMENT-LIKE PROTEIN 1)	726	THY		5.38	81.97	0.0	0.0	100.0	89.0		28.3* DNA.plastid nucleoid interacting	chloroplast	Y	C	plastid nucleoid	

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AT3G16140	613	AT3G16140.1	PSAH-1 (photosystem I subunit H-1)	145	THY	Ch/Th	9.95	15.21	2.6447888719489 1	0.0	97.355211128051 1	244.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	undefined	Y	C	thylakoid-integral	
AT3G16240	614	AT3G16240.1	DELTA-TIP (delta tonoplast integral protein); water channel	250	THY-ENV	Ch/E & other	5.3	25.02	22.892443129879 9	0.0	77.107556870120 1	9.0	transporter aquaporin	34.19.2 transport.Major Intrinsic Proteins.TIP	secreted		S	-	6.0
AT3G16290	615	AT3G16290.1	EMB2083 (EMBRYO DEFECTIVE 2083); ATPase/metallopeptidase	876	ENV	Ch/E/IM	9.27	99.86	100.0	0.0	0.0	59.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	undefined		C	plastid	2.0
AT3G16950	616	AT3G16950.1	LPD1 (LIPOAMIDE DEHYDROGENASE 1)	570	ENV-STR	Ch/E & other	8.13	60.75	53.243379731174 9	41.632699921228 1	5.123920347597 0 2	50.0	metabolism lipid	11.1 lipid metabolism.FA synthesis and FA elongation	chloroplast	Y	C	plastid	
AT3G17810	617	AT3G17810.1	dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein	426	STR		6.37	46.84	0.0	100.0	0.0	15.0		23.2 nucleotide metabolism.degradation	chloroplast	Y	C	plastid	
AT3G17830	618	AT3G17830.1	DNAJ heat shock family protein	517	ENV	Ch/E/IM	9.49	57.26	100.0	0.0	0.0	5.0	chaperone and protease	20.2.1 stress.abiotic.heat	chloroplast	Y	C	-	1.0

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AT3G17970	619	AT3G17970.1	ATTOC64-III (ARABIDOPSIS THALIANA TRANSLOCON AT THE OUTER MEMBRANE OF CHLOROPLASTS 64-III); binding / carbon-nitrogen ligase, with glutamine as amido-N-donor	589	ENV	Ch/E & other	8.61	64.02	100.0	0.0	0.0	55.0	protein targeting Toc	26.33* misc.tetratricopeptide repeat (TPR) unknown function	undefined		S	-	
AT3G18420	620	AT3G18420.1	tetratricopeptide repeat (TPR)-containing protein	316	ENV	Ch/E & Ch/S	5.24	35.63	100.0	0.0	0.0	26.0	unknown	26.33* misc.tetratricopeptide repeat (TPR) unknown function	chloroplast	Y	C	-	
AT3G18890	621	AT3G18890.1	binding / catalytic/ coenzyme binding	641	THY-ENV	Ch/E & Ch/Th	8.27	68.34	25.279244045656 3	0.0	74.720755954343 7	89.0	protein targeting Tic	20.2.5 stress.abiotic.light	chloroplast	Y	C	thylakoid	
AT3G18970	622	AT3G18970.1	pentatricopeptide (PPR) repeat-containing protein	472			9.03	52.55	0.0	100.0	0.0	2.0		35.1.5 not assigned. no ontology. pentatricopeptide (PPR) repeat-containing protein	undefined		M	-	

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AT3G19170	623	AT3G19170.1	ATPREP1/ATZNMP (PRESEQUENCE PROTEASE 1); metalloendopeptidase	1080	STR		5.47	121.01	0.0	100.0	0.0	426.0		29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	mitochondria; plastid stroma	
AT3G19480	624	AT3G19480.1	D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative	588	STR		8.41	62.12	0.0	100.0	0.0	55.0		13.1.5.1.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	chloroplast	Y	C	plastid stroma	
AT3G19820	625	AT3G19820.1	DWF1 (DIMINUTO 1); catalytic	561	ENV	other	7.98	65.39	100.0	0.0	0.0	4.0	metabolism hormone	17.3.1.2.8 hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF1	undefined		M	-	1.0
AT3G20230	626	AT3G20230.1	50S ribosomal protein L18 family	187			10.24	21.12	0.0	100.0	0.0	4.0		29.2.1.1.3.2.18 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L18	chloroplast	Y	C	plastid ribosome	
AT3G20320	627	AT3G20320.1	TGD2 (TRIGALACTOSYLDIACYLGLYCEROL2)	381	ENV	Ch/E/IM	8.9	41.63	94.541058201974 2	0.0	5.4589417980257 9	116.0	transporter lipids	11.15* lipid metabolism.transport	chloroplast	Y	C	envelope-inner	1.0

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AT3G20330	628	AT3G20330.1	aspartate carabmoyltransferase, chloroplast / aspartate transcarbamylase / ATCase (PYRB)	390	STR		6.2	43.16	0.0	100.0	0.0	57.0		23.1.1.2 nucleotide metabolism.synthesis.pyrimidine.aspartate transcarbamoylase	chloroplast	Y	C	plastid stroma	
AT3G20390	629	AT3G20390.1	endoribonuclease L-PSP family protein	187	ENV-STR	Ch/E & Ch/S	8.52	19.81	57.810045970493 5	42.189954029506 5	0.0	42.0	RNA metabolism?	27.1 RNA.processing; 27.1.19 RNA.processing.ribonucleases	undefined	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT3G21110	630	AT3G21110.1	PUR7 (PURIN 7); phosphoribosylaminoimidazolesuccinocarboxamide synthase	411	STR		6.06	46.06	0.0	100.0	0.0	12.0		23.1.2.7 nucleotide metabolism.synthesis.purine.SAICAR synthetase	undefined	Y	C	plastid stroma	
AT3G21200	631	AT3G21200.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN79599.1); contains InterPro domain FMN-binding split barrel, related (InterPro: IPR009002)	317			5.65	35.46	0.0	100.0	0.0	6.0		35.2 not assigned. unknown	chloroplast	Y	C	-	
AT3G21580	632	AT3G21580.2	cobalt ion transmembrane transporter	205	ENV	Ch/E/IM	9.71	22.87	100.0	0.0	0.0	1.0	transporter ABC Co ?	34.12 transport. metal	chloroplast	Y	M	-	6.0

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AT3G22150	633	AT3G22150.1	pentatricopeptide (PPR) repeat-containing protein	820	ENV	Ch/E ?	6.94	91.85	100.0	0.0	0.0	4.0	RNA Binding ?	26.54* misc.pentatricopeptide (PPR) repeat-containing protein	chloroplast	Y	C	-	
AT3G22890	634	AT3G22890.1	APS1 (ATP sulfurylase 3)	463	STR		6.33	51.46	0.0	100.0	0.0	106.0		14.1 S-assimilation.APS	chloroplast	Y	C	plastid stroma	
AT3G22960	635	AT3G22960.1	PKP-ALPHA/PKP1 (PLASTIDIAL PYRUVATE KINASE 1); pyruvate kinase	596	STR		5.64	65.13	0.0	100.0	0.0	124.0		11.1.30 lipid metabolism.FA synthesis and FA elongation.pyruvate kinase	chloroplast	Y	C	plastid stroma	
AT3G23400	636	AT3G23400.1	plastid-lipid associated protein PAP / fibrillin family protein	284	THY-ENV	Ch	5.82	30.45	37.097719173072 2	0.0	62.902280826927 8	118.0	PAP_fibrillin	26.31* misc.fibrillins	chloroplast	Y	C	plastoglobules; thylakoid-peripheral-stromal-side	
AT3G23700	637	AT3G23700.1	S1 RNA-binding domain-containing protein	392	STR		5.39	42.75	0.0	100.0	0.0	55.0		35.1.14 not assigned.no ontology.S RNA-binding domain-containing protein	chloroplast	Y	C	plastid stroma	
AT3G23710	638	AT3G23710.1	chloroplast inner membrane import protein Tic22, putative	313	ENV-STR	Ch/E/IM	8.43	34.57	61.517808107723 3	38.482191892276 7	0.0	3.0	protein targeting Tic	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	-	

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AT3G23790	639	AT3G23790.1	AMP-binding protein, putative	722	ENV	Ch/E/IM	8.73	81.14	100.0	0.0	0.0	10.0	metabolism lipid	11.1.8 lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	chloroplast	Y	C	-	
AT3G23940	640	AT3G23940.1	dehydratase family	608	STR		5.85	64.91	0.0	100.0	0.0	132.0		35.1 not assigned. no ontology	chloroplast	Y	C	plastid stroma	
AT3G24430	641	AT3G24430.1	HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP binding	532	STR		5.91	57.76	0.0	100.0	0.0	34.0		29.8 protein assembly and cofactor ligation	chloroplast	Y	C	plastid stroma	
AT3G24590	642	AT3G24590.1	signal peptidase I family protein	291			5.73	32.55	0.0	0.0	100.0	1.0		29.9* protein.processing	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT3G25660	643	AT3G25660.1	glutamyl-tRNA(Gln) amidotransferase, putative	537	STR		6.16	57.18	0.0	100.0	0.0	22.0		29.1.50* protein.aa activation.glutamate-tRNA amidotransferase	chloroplast	Y	C	mitochondria; plastid stroma	

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AT3G25680	644	AT3G25680.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42077.1); contains InterPro domain S-layer homology region (InterPro:IPR001119)	558	ENV	Ch/E/IM	5.18	63.05	100.0	0.0	0.0	49.0	unknown	35.2 not assigned. unknown	undefined	Y	C	-	1.0
AT3G25690	645	AT3G25690.1	CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)	1004	ENV	Ch/E/OM	5.43	111.91	100.0	0.0	0.0	2.0	plastid positioning	35.1.41 not assigned. no ontology. hydroxyproline rich proteins	secreted		S	envelope-outer	
AT3G25760	646	AT3G25760.1	AOC1 (ALLENE OXIDE CYCLASE 1)	254	ENV	Ch/E & Ch/Th	9.11	27.8	82.5636826982338	8.6078908927825 1	8.8284264089836 5	13.0	metabolism hormone jasmonate	17.7.1.3 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	chloroplast	Y	C	plastid	

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AT3G25770	647	AT3G25770.1	AOC2 (ALLENE OXIDE CYCLASE 2)	253	ENV-STR	Ch/E & Ch/Th	6.9	27.63	70.371143509358 4	18.341815236817 7	11.287041253824	12.0	metabolism hormone jasmonate	17.7.1.4 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase cyclase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT3G25780	648	AT3G25780.1	AOC3 (ALLENE OXIDE CYCLASE 3)	258	ENV	Ch/E/IM	9.19	28.39	100.0	0.0	0.0	3.0	metabolism hormone jasmonate	17.7.1.4 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase cyclase	chloroplast	Y	C	plastid	
AT3G25860	649	AT3G25860.1	LTA2 (PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE); dihydrolipoyllysine-residue acetyltransferase	480	ENV-THY	Ch/E & other	8.33	50.08	54.185613669286 6	20.982972026124 1	24.831414304589 3	81.0	metabolism lipid	11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	chloroplast	Y	C	plastid	
AT3G25920	650	AT3G25920.1	RPL15 (ribosomal protein L15)	277	STR-ENV	Ch/S	10.77	29.7	21.902879659449 5	78.097120340550 5	0.0	158.0	translation stroma	29.2.1.1.1.2.15 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L15	chloroplast	Y	C	plastid ribosome	
AT3G26060	651	AT3G26060.1	ATPRXQ; antioxidant/ peroxiredoxin	216	THY-ENV	Ch	9.53	23.67	24.074755548357 3	0.627494021154847	75.297750430487 8	72.0	redox	21.5 redox.peiredoxins	chloroplast	Y	C	plastid	

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AT3G26070	652	AT3G26070.1	plastid-lipid associated protein PAP / fibrillin family protein	242	THY	Ch	9.7	27.16	13.782973726184 4	0.0	86.217026273815 6	28.0	PAP_fibrillin	26.31* misc.fibrillins	undefined	Y	C	thylakoid-peripheral-stromal-side	
AT3G26520	653	AT3G26520.1	TIP2 (TONOPLAST INTRINSIC PROTEIN 2); water channel	253	ENV-THY	other	4.91	25.84	83.859436586073 3	0.0	16.140563413926 7	6.0	transporter aquaporin	34.19.2 transport. Major Intrinsic Proteins. TIP	undefined			-	6.0
AT3G26570	654	AT3G26570.1	PHT2;1 (phosphate transporter 2;1)	613	ENV	Ch/E/IM	9.26	64.78	100.0	0.0	0.0	90.0	transporter Pi	34.7 transport. phosphate	undefined	Y		envelope-inner-integral	12.0
AT3G26650	655	AT3G26650.1	GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase	396	STR-ENV	Ch	7.61	42.49	18.675757760825 1	76.095800417725 7	5.228441821449 1 7	2192.0	metabolism carbon	1.3.4 PS.calvincyle.GAP	chloroplast	Y	C	plastid stroma	
AT3G26710	656	AT3G26710.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO49107.1)	267			9.79	30.1	0.0	0.0	100.0	6.0		35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	3.0

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AT3G26900	657	AT3G26900.1	shikimate kinase family protein	280			5.04	30.47	0.0	100.0	0.0	3.0		13.1.6.1.5 amino acid metabolism.synthesis.aromatic aa.chorismate.shikimate kinase	chloroplast	Y	C	plastid stroma	
AT3G27160	658	AT3G27160.1	GHS1 (GLUCOSE HYPERSENSITIVE 1); structural constituent of ribosome	183	STR-THY	Ch/S	9.44	20.91	9.2660237346249 7	55.065040300093	35.668935965282	36.0	translation stroma	29.2.1.1.3.1.21 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S21	chloroplast	Y	C	plastid ribosome	
AT3G27740	659	AT3G27740.1	CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing)	430	STR		5.68	47.05	0.0	100.0	0.0	13.0		23.1.1.1 nucleotide metabolism.synthesis.pyrimidine.carbamoyl phosphate synthetase	chloroplast	Y	C	plastid stroma	
AT3G27830	660	AT3G27830.1	RPL12-A (RIBOSOMAL PROTEIN L12-A); structural constituent of ribosome	191	STR-ENV	Ch/S & Ch/Th	5.5	20.07	37.78794073807	50.090214291457 7	12.121844970472 3	165.0	translation stroma	29.2.1.1.1.2.12 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L12	chloroplast	Y	C	plastid ribosome	

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AT3G27890	661	AT3G27890.1	NQR (NADPH: QUINONE OXIDOREDUCTASE); FMN reductase	196	STR		6.84	21.55	0.0	100.0	0.0	27.0		35.1 not assigned. no ontology	undefined		M	-	
AT3G27925	662	AT3G27925.1	DEGP1 (DEGP PROTEASE 1); serine-type peptidase	439	THY	Lum	5.99	46.67	0.0	13.978739289650 5	86.021260710349 5	38.0		29.5.5 protein.degradation.serine protease	undefined	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT3G28220	663	AT3G28220.1	meprin and TRAF homology domain-containing protein / MATH domain-containing protein	370	ENV	Ch/E ?	8.59	42.88	100.0	0.0	0.0	2.0	chaperone and protease ?	35.2 not assigned. unknown	other (e.g. cytoplasm)			-	1.0
AT3G28345	664	AT3G28345.1	ABC transporter family protein	1240			8.21	135.64				1.0		34.16 transport. ABC transporters and multidrug resistance systems	other (e.g. cytoplasm)			-	11.0
AT3G28710	665	AT3G28710.1	H+-transporting two-sector ATPase, putative	351	ENV	other	5.04	40.79	100.0	0.0	0.0	1.0	transporter ATPase	34.1.1 transport. p- and v-ATPases .H+-transporting two-sector ATPase	undefined			-	

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AT3G28760	666	AT3G28760.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO14940.1); contains InterPro domain 3-dehydroquinate synthase, prokaryotic-type (InterPro: IPR002812)	422			6.69	47.05	0.0	100.0	0.0	4.0		13.1.6.1 amino acid metabolism.synthesis.aromatic aa.chorismate	undefined	Y	C	-	
AT3G29185	667	AT3G29185.1	similar to hypothetical protein MtrDRAFT_AC147482g2v2 [Medicago truncatula] (GB:ABD32485.1)	396			5.24	44.67	0.0	100.0	0.0	8.0		35.2 not assigned. unknown	chloroplast	Y	C	-	1.0
AT3G29320	668	AT3G29320.1	glucan phosphorylase, putative	962	STR	Ch/S	5.35	108.58	4.7579493181803 9	95.242050681819 6	0.0	119.0	metabolism carbon	2.2.2.2 major CHO metabolism.degradation.starch.starch phosphorylase	undefined	Y	C	plastid stroma	
AT3G32930	669	AT3G32930.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO22035.1)	249	ENV	Ch/E/IM	9.6	27.43	100.0	0.0	0.0	7.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	

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AT3G42050	670	AT3G42050.1	vacuolar ATP synthase subunit H family protein	441	ENV	other	6.57	50.28	100.0	0.0	0.0	3.0	transporter ATPase	34.1.1 transport. p- and v-ATPases .H+-transporting two-sector ATPase	other (e.g. cytoplasm)			-	
AT3G43520	671	AT3G43520.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26240.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ63811.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349	240	ENV	Ch/E/IM	9.13	24.76	100.0	0.0	0.0	25.0	unknown	35.1.40 not assigned. no ontology. glycine rich proteins	chloroplast	Y	C	plastid	4.0
AT3G44880	672	AT3G44880.1	ACD1 (ACCELERATED CELL DEATH 1)	537	ENV-THY	Ch/E/IM	7.19	60.75	77.153932309513	0.0	22.846067690487	18.0	metabolism vitamin and pigment	19.50* tetrapyrrole degradation	chloroplast	Y	C	envelope-inner	

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AT3G44890	673	AT3G44890.1	RPL9 (ribosomal protein L9); structural constituent of ribosome	197	STR-ENV	Ch/S	9.68	22.13	26.787079018215 8	60.323538308565 2	12.88938 2673219	129.0	translation stroma	29.2.1.1.1.2.9 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L9	chloroplast	Y	C	plastid ribosome	
AT3G45140	674	AT3G45140.1	LOX2 (LIPOXYGENASE 2)	896	STR	Ch/E & Ch/S	5.42	102.04	9.2650260327746 6	86.276837044847 2	4.4581369223781 4	872.0	metabolism lipid	17.7.1.2 hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	chloroplast	Y	C	plastid stroma	
AT3G45450	675	AT3G45450.1	Clp amino terminal domain-containing protein	341	STR-ENV	Ch	8.73	37.34	37.423354940263 1	56.574195969732	6.0024454627637 6	39.0	chaperone and protease	29.3.99 protein.targeting.unknown	undefined			-	
AT3G45890	676	AT3G45890.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13770.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23851.1); contains InterPro domain Protein of unknown function DUF647 (InterPro:IPR006968)	608	ENV	Ch/E/IM	6.4	66.38	100.0	0.0	0.0	12.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	3.0

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AT3G45980	677	AT3G45980.1	HTB9; DNA binding	150	THY-STR		10.02	16.43	0.0	39.394425184858 6	60.605574815141 4	12.0		28.1.3 DNA.synthesis/chromatin structure.histone	other (e.g. cytoplasm)			nucleus	
AT3G46060	678	AT3G46060.1	ARA3; GTP binding	216	ENV	Ch/E ?	7.64	23.83	100.0	0.0	0.0	4.0	signalling / SNARE effector	30.5 signalling.G-proteins	undefined			plasma membrane	
AT3G46520	679	AT3G46520.1	ACT12 (ACTIN-12); structural constituent of cytoskeleton	377	ENV-STR	Ch/E & other	5.37	41.79	54.523820970145 7	45.476179029854 3	0.0	23.0	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT3G46740	680	AT3G46740.1	TOC75-III (translocon outer membrane complex 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	818	ENV	Ch/E/OM	8.93	89.19	96.213707931402 1	0.0	3.786292068597 8	296.0	protein targeting Toc	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope-outer	
AT3G46780	681	AT3G46780.1	PTAC16 (PLASTID TRANSCRIPTIONALLY ACTIVE18); binding / catalytic	510	THY-ENV	Ch/E & Ch/Th	8.9	54.35	21.999633654543 3	0.0	78.000366345456 7	320.0	protein targeting Tic ?	28.3* DNA.plastid nucleoid interacting	undefined	Y	C	thylakoid	
AT3G46980	682	AT3G46980.1	transporter-related	533	ENV	Ch/E/IM	9.79	58.24	100.0	0.0	0.0	3.0	transporter Pi ?	34.7 transport.phosphate	undefined			plastid	12.0

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AT3G47010	683	AT3G47010.1	hydrolase, hydrolyzing O-glycosyl compounds	609	ENV	Ch/E ?	5.27	63.0	100.0	0.0	0.0	2.0	hydrolase ?	10.6.1 cell wall.degradation.cellulases and beta-1,4-glucanases	other (e.g. cytoplasm)			-	
AT3G47060	684	AT3G47060.1	FTSH7 (FtsH protease 7); ATP-dependent peptidase/ ATPase/ metalloprotease	802	ENV	Ch/E/IM	8.3	87.8	100.0	0.0	0.0	12.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	undefined	Y	C	-	2.0
AT3G47070	685	AT3G47070.1	similar to unknown [Populus trichocarpa] (GB:ABK95428.1)	100	THY		9.74	10.53	0.0	0.0	100.0	69.0		1.1.30 PS.lightreaction.state transition	undefined			thylakoid-peripheral-stromal-side	
AT3G56910	746	AT3G56910.1	PSRP5 (PLASTID-SPECIFIC 50S RIBOSOMAL PROTEIN 5)	148	ENV-STR	Ch/S & Ch/Th	10.85	16.36	61.517808107723 3	38.482191892276 7	0.0	3.0	translation stroma	29.2.1.1.1.2.85 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.PSRP5	chloroplast	Y	C	plastid ribosome	
AT3G47470	686	AT3G47470.1	LHCA4 (Photosystem I light harvesting complex gene 4); chlorophyll binding	251	THY	Ch	6.21	27.73	2.9655833037916 4	0.0	97.034416696208 4	319.0	PS LHC	1.1.2.1 PS.lightreaction.photosystem I.LHC-I	chloroplast	Y	C	thylakoid-integral	

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AT3G47520	687	AT3G47520.1	MDH (MALATE DEHYDROGENASE); malate dehydrogenase	403	Mix	Ch/S & other	8.66	42.4	44.772698935577	43.626854140259 7	11.600446924163 3	313.0	metabolism carbon	8.2.99 TCA / org.transformation.other organic acid transformaitons.misc	chloroplast	Y	C	plastid stroma	
AT3G47590	688	AT3G47590.1	esterase/lipase/thioesterase family protein	309			7.73	35.04	0.0	100.0	0.0	6.0		35.1 not assigned.no ontology	undefined	Y		-	
AT3G47650	689	AT3G47650.1	bundle-sheath defective protein 2 family / bsd2 family	136			8.0	14.54	0.0	100.0	0.0	7.0		33.99 development.unspecified	chloroplast	Y	C	plastid stroma	
AT3G47860	690	AT3G47860.1	apolipoprotein D-related	353			6.36	39.11	0.0	0.0	100.0	7.0		11.6 lipid metabolism.lipid transfer proteins etc	chloroplast	Y	C	thylakoid	
AT3G48110	691	AT3G48110.1	EDD1 (EMBRYO-DEFECTIVE-DEVELOPMENT 1)	1067	STR		5.69	119.77	0.0	100.0	0.0	39.0		29.1.14 protein.aa activation.glycine-tRNA ligase	chloroplast	Y	C	mitochondria; plastid stroma	
AT3G48420	692	AT3G48420.1	haloacid dehalogenase-like hydrolase family protein	319	STR		8.3	34.24	0.0	100.0	0.0	69.0		35.1 not assigned.no ontology	chloroplast	Y	C	plastid stroma	

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AT3G48500	693	AT3G48500.1	PDE312/PTAC10 (PIGMENT DEFECTIVE 312); RNA binding / unfolded protein binding	668	STR		4.96	78.81	0.0	100.0	0.0	11.0		28.3* DNA.plastid nucleoid interacting	chloroplast	Y	C	-	
AT3G48560	694	AT3G48560.1	CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1)	670	STR		6.19	72.58	0.0	100.0	0.0	16.0		13.1.4.1.1 amino acid metabolism.synthesis.branched chain group.common.acetolactate synthase	chloroplast	Y	C	plastid stroma	
AT3G48730	695	AT3G48730.1	GSA2 (GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2); glutamate-1-semialdehyde 2,1-aminomutase	472	STR	Ch/E & Ch/S	7.01	50.14	5.8978196282442 4	93.15621184218 6	0.94596918753715	450.0	metabolism vitamin and pigment	19.3 tetrapyrrole synthesis.GSA	chloroplast	Y	C	plastid stroma	
AT3G48870	696	AT3G48870.1	ATCLPC (CASEINOLYTIC PROTEASE C); ATP binding / ATPase	952	ENV-STR	Ch & other	6.06	105.77	62.448263991100 9	32.653914032016 7	4.8978219768823 4	1629.0	chaperone and protease	29.5.5 protein.degradation.serine protease	undefined		C	plastid stroma	

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AT3G48990	697	AT3G48990.1	AMP-dependent synthetase and ligase family protein	514	STR		6.08	55.54	0.0	100.0	0.0	11.0		11.1.8 lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	undefined			-	2.0
AT3G49140	698	AT3G49140.1	binding	1215			4.94	135.91	0.0	100.0	0.0	8.0		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	undefined		M	-	
AT3G49560	699	AT3G49560.1	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	261	ENV	Ch/E/OM	9.49	27.98	100.0	0.0	0.0	73.0	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane	other (e.g. cytoplasm)			envelope	3.0
AT3G49680	700	AT3G49680.1	ATBCAT-3/BCAT3 (BRANCHED-CHAIN AMINOTRANSFERASE 3); branched-chain-amino-acid transaminase/ catalytic	413	STR		8.32	44.97	0.0	100.0	0.0	32.0		13.1.4.1.4 amino acid metabolism.synthesis.branched chain group.common.branched-chain amino acid aminotransferase	chloroplast	Y	C	plastid stroma	

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AT3G50820	701	AT3G50820.1	PSBO-2/PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); oxygen evolving/ poly(U) binding	331	THY	Ch/Th/Lum	5.92	35.01	5.9109364909835 4	5.2619124409901 4	88.827151068026 3	526.0	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT3G51140	702	AT3G51140.1	heat shock protein binding	278	ENV	Ch/E/IM	10.66	31.53	96.144762448164 5	0.0	3.8552375518355 1	51.0	signalling?	35.2 not assigned. unknown	chloroplast	Y	C	-	4.0
AT3G51510	703	AT3G51510.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO14460.1)	181			6.2	19.84	0.0	0.0	100.0	3.0		35.2 not assigned. unknown	chloroplast		C	thylakoid	2.0
AT3G51600	704	AT3G51600.1	LTP5 (LIPID TRANSFER PROTEIN 5); lipid transporter	118			10.43	12.49				1.0		11.6 lipid metabolism.lipid transfer proteins etc	secreted		S	-	
AT3G51800	705	AT3G51800.1	ATG2 (G2p-related protein); metalloexopeptidase	392			6.35	42.98	0.0	100.0	0.0	3.0		29.5.7 protein.degradation.metalloprotease	other (e.g. cytoplasm)			-	
AT3G51820	706	AT3G51820.1	ATG4/CHLG/G4 (CHLOROPHYLL SYNTHASE); chlorophyll synthetase	387	THY		8.52	41.88	0.0	0.0	100.0	12.0		19.15 tetrapyrrole synthesis.chlorophyll synthase	chloroplast	Y	C	thylakoid	8.0

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AT3G51870	707	AT3G51870.1	mitochondrial substrate carrier family protein	381	ENV	Ch/E/IM	9.75	41.81	100.0	0.0	0.0	4.0	transporter MCF Ca/X ?	34.99 transport.misc	undefined	Y	C	-	2.0
AT3G52150	708	AT3G52150.1	RNA recognition motif (RRM)-containing protein	253	STR	Ch	8.94	27.74	14.504205202124 5	77.120850246708 3	8.3749445511672 1	107.0	translation stroma ?	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	chloroplast	Y	C	plastid ribosome ; thylakoid-peripheral-stromal-side	
AT3G52180	709	AT3G52180.1	ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase	379	STR		6.11	42.62	0.0	100.0	0.0	35.0		2.2.2.2 major CHO metabolism.degradation.starch.starch phosphorylase	undefined	Y	C	plastid stroma	
AT3G52230	710	AT3G52230.1	similar to unknown [Populus trichocarpa] (GB:ABK93315.1)	145	ENV	Ch/E & Ch/Th	4.51	16.12	93.776122668184 3	0.0	6.2238773318156 6	69.0	transporter ion channel	35.2 not assigned.unknown	undefined			envelope -outer	
AT3G52380	711	AT3G52380.1	CP33 (PIGMENT DEFECTIVE 322); RNA binding	329	STR	Ch/E & Ch/S	4.61	35.74	5.059098649412 6 9	94.940901350587 3	0.0	83.0	RNA Binding ?	27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT3G52750	712	AT3G52750.1	FTSZ2-2 (FtsZ2-2); structural molecule	473	STR-THY		5.67	50.31	0.0	61.102590566953 8	38.897409433046 2	41.0		31.2.5 cell.division.plastid	undefined			plastid stroma	

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AT3G52880	713	AT3G52880.1	ATMDAR1 (MONODEHYDROASCORBATE REDUCTASE 1); monodehydroascorbate reductase (NADH)	434			6.41	46.48	0.0	100.0	0.0	2.0		21.2.1 redox.ascorbate and glutathione.ascorbate	secreted			peroxisome	
AT3G52930	714	AT3G52930.1	fructose-bisphosphate aldolase, putative	358			6.04	38.54	0.0	100.0	0.0	3.0		4.7 glycolysis.aldolase	undefined			cytosol	
AT3G52960	715	AT3G52960.1	peroxiredoxin type 2, putative	234	STR-ENV	Ch	9.11	24.68	39.862647390635 9	55.874891955304 4	4.2624606540597 2	201.0	redox	21.5 redox.peri redoxins	chloroplast	Y	C	plastid stroma	
AT3G53130	716	AT3G53130.1	LUT1 (LUTEIN DEFICIENT 1); oxygen binding	539	ENV	Ch/E/IM	6.04	60.55	100.0	0.0	0.0	16.0	metabolism vitamin and pigment	16.1.4 secondary metabolism.isoprenoids.carotenoids	chloroplast	Y	C	plastid	
AT3G53220	717	AT3G53220.1	thioredoxin family protein	126	ENV	CH/E ?	5.9	14.41	100.0	0.0	0.0	2.0	redox	21.1 redox.thioredoxin	other (e.g. cytoplasm)			-	
AT3G53460	718	AT3G53460.1	CP29 (chloroplast 29 kDa ribonucleoprotein); RNA binding / poly(U) binding	342	THY-STR	Ch/S	5.24	36.0	6.4954502673199 5	37.246000850904	56.258548881776 1	125.0	RNA Binding	27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT3G53560	719	AT3G53560.1	chloroplast lumen common family protein	340	ENV	Ch/E & Ch/Th	6.58	38.66	92.747756554005 6	7.252243445994 3 8	0.0	42.0	unknown	35.1 not assigned. no ontology	undefined	Y	C	plastid	

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AT3G53580	720	AT3G53580.1	diaminopimelate epimerase family protein	362	STR		5.45	38.98	0.0	100.0	0.0	32.0		13.1.3.5.4 amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate epimerase	chloroplast	Y	C	plastid stroma	
AT3G53900	721	AT3G53900.1	uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative	231	STR		6.31	25.16	0.0	100.0	0.0	45.0		23.3.1.3 nucleotide metabolism.salvage.phosphoribosyltransferases.upp	chloroplast		C	plastid stroma	
AT3G54050	722	AT3G54050.1	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	417	STR	Ch/S	5.24	45.16	7.9758552486997 3	92.024144751300 3	0.0	449.0	metabolism carbon	1.3.7 PS.calvin cyle.FBPase	chloroplast	Y	C	plastid stroma	
AT3G54090	723	AT3G54090.1	pfkB-type carbohydrate kinase family protein	471			5.76	53.78	0.0	100.0	0.0	5.0		2.2.1.1 major CHO metabolism.degradation.sucrose.fructokinase	undefined	Y	C	-	

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AT3G54170	724	AT3G54170.1	ATFIP37 (ARABIDOPSIS THALIANA FKBP12 INTERACTING PROTEIN 37)	330			4.93	37.21	0.0	100.0	0.0	2.0		31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT3G54210	725	AT3G54210.1	ribosomal protein L17 family protein	211	ENV-STR	Ch/S	11.38	23.48	53.016941031420 6	46.983058968579 4	0.0	30.0	translation stroma	29.2.1.1.1.2.17 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L17	chloroplast	Y	C	plastid ribosome	
AT3G54400	726	AT3G54400.1	aspartyl protease family protein	425			9.3	45.47	0.0	0.0	100.0	4.0		27.3.99 RNA.regulation of transcription.unclassified	undefined		S	-	
AT3G54640	727	AT3G54640.1	TSA1 (TRYPTOPHAN SYNTHASE ALPHA CHAIN); tryptophan synthase	312			6.76	33.2	0.0	100.0	0.0	5.0		13.1.6.5.5 amino acid metabolism.synthesis.aromatic aa.tryptophan.tryptophan synthase	chloroplast	Y	C	plastid stroma	
AT3G54660	728	AT3G54660.1	GR (GLUTATHIONE REDUCTASE); glutathione-disulfide reductase	565	STR	Ch & other	7.96	60.85	10.500828297794 9	89.499171702205 1	0.0	120.0	redox	21.2.2 redox.ascorbate and glutathione.glutathione	chloroplast	Y	C	plastid stroma	
AT3G54890	729	AT3G54890.1	LHCA1; chlorophyll binding	241	THY	Ch/Th	6.21	25.99	7.732013 5014273 1	0.0	92.26798 6498572 7	181.0	PS LHC	1.1.2.1 PS.lightreaction.photosystem I.LHC-I	chloroplast	Y	C	thylakoid-integral	1.0

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AT3G54900	730	AT3G54900.1	CXIP1 (CAX INTERACTING PROTEIN 1)	173	STR-ENV	Ch/E ?	8.66	19.31	26.212628759875	73.787371240125	0.0	14.0	redox	21.5 redox.peiredoxins	chloroplast	Y	C	plastid	
AT3G55010	731	AT3G55010.1	ATPURM/PUR5; phosphoribosylformylglycinamidine cyclo-ligase	389	STR		5.31	41.5	0.0	100.0	0.0	18.0		23.1.2.5 nucleotide metabolism.synthesis.purine.AIR synthase	chloroplast	Y	C	plastid stroma	
AT3G55030	732	AT3G55030.1	PGPS2 (phosphatidylglycerolphosphate synthase 2); CDP-alcohol phosphatidyltransferase/ CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	233	ENV	Ch/E/IM	9.61	25.22	100.0	0.0	0.0	4.0	metabolism lipid	11.3.3 lipid metabolism.Phospholipid synthesis.phosphatidate cytidylyltransferase	other (e.g. cytoplasm)	Y		-	4.0
AT3G55040	733	AT3G55040.1	In2-1 protein, putative	292	STR		6.77	33.05	0.0	100.0	0.0	29.0		26.9 misc.glutathione S transferases	chloroplast	Y	C	plastid stroma	
AT3G55250	734	AT3G55250.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO14780.1)	277	ENV-STR	Ch/E & other	5.85	31.24	68.066144160060 3	31.933855839939 7	0.0	25.0	signalling Calcium ?	35.2 not assigned. unknown	chloroplast	Y	C	plastid	1.0

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AT3G55330	735	AT3G55330.1	PPL1 (PSBP-LIKE PROTEIN 1); calcium ion binding	230		Lum	9.36	25.62	0.0	0.0	100.0	7.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT3G55400	736	AT3G55400.1	OVA1 (OVULE ABORTION 1); ATP binding / aminoacyl-tRNA ligase	616	STR		6.15	69.27	0.0	100.0	0.0	26.0		29.1.10 protein.aa activation.methionine-tRNA ligase	chloroplast	Y	C	mitochondria; plastid stroma	
AT3G55440	737	AT3G55440.1	ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); triose-phosphate isomerase	254	STR		5.39	27.16	0.0	100.0	0.0	21.0		4.8 glycolysis.TPI	undefined			not plastid	
AT3G55610	738	AT3G55610.1	P5CS2 (DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHASE 2); catalytic/ glutamate 5-kinase/ glutamate-5-semialdehyde dehydrogenase/ oxidoreductase	726			6.34	78.87	0.0	100.0	0.0	2.0		13.1.2.2.1 amino acid metabolism.synthesis.glutamate family.proline.delta 1-pyrroline-5-carboxylate synthetase	undefined			-	

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AT3G55760	739	AT3G55760.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G42430.1); similar to hypothetical protein [Trifolium pratense] (GB:BAE71279.1)	578	STR		5.31	65.57	0.0	100.0	0.0	22.0		35.2 not assigned. unknown	undefined	Y	C	plastid	
AT3G55800	740	AT3G55800.1	SBPASE (SEDOHEPTULOSE-BISPHOSPHATASE); phosphoric ester hydrolase/ sedoheptulose-bisphosphatase	393	STR	Ch/S	6.17	42.41	14.069326114032 7	85.285924768874 7	0.644749117092583	604.0	metabolism carbon	1.3.9 PS.calvin cyle.sedu heptulose bisphosphatase	chloroplast	Y	C	plastid stroma	
AT3G56090	741	AT3G56090.1	ATFER3 (FERRITIN 3); ferric iron binding	259	STR		5.54	28.83	0.0	100.0	0.0	15.0		15.2 metal handling. binding, chelation and storage	chloroplast	Y	C	plastid stroma	
AT3G56130	742	AT3G56130.1	biotin/lipoyl attachment domain-containing protein	281			8.86	29.57	0.0	100.0	0.0	8.0		11.1.1 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	chloroplast	Y	C	plastid	

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AT3G56160	743	AT3G56160.1	bile acid:sodium symporter	436	ENV	Ch/E/IM	9.91	46.53	100.0	0.0	0.0	9.0	transporter Na/X ?	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	7.0
AT3G56650	744	AT3G56650.1	thylakoid lumenal 20 kDa protein	262	THY	Lum	9.29	28.63	0.0	13.978739289650 5	86.021260710349 5	19.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT3G56690	745	AT3G56690.1	CIP111 (CAM INTERACTING PROTEIN 111); ATPase/calmodulin binding	1022	ENV	Ch/E & Ch/Th	6.05	111.52	100.0	0.0	0.0	5.0	signalling Calcium ?	30.3 signalling.calcium	undefined	Y	C	-	
AT3G56940	747	AT3G56940.1	AT103 (DICARBOXYLATE DIIRON 1)	409	ENV-THY	Ch/E & Ch/Th	8.55	47.63	63.853165785556 9	0.0	36.146834214443 1	94.0	metabolism vitamin and pigment	19.12 tetrapyrrole synthesis.magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	chloroplast	Y	C	envelope-inner-peripheral-stromal-side; thylakoid-peripheral-stromal-side	
AT3G57050	748	AT3G57050.1	CBL (CYSTATHIONINE BETA-LYASE)	464	STR		6.9	50.43	0.0	100.0	0.0	12.0		13.1.3.4.2 amino acid metabolism.synthesis.aspartate family.methionine.cystathionine beta-lyase	chloroplast	Y	C	plastid	

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AT3G57090	749	AT3G57090.1	BIGYIN; binding	170	ENV	Ch/E ?	5.54	18.69	100.0	0.0	0.0	2.0	RNA binding ?	26.33* misc.tetratricopeptide repeat (TPR) unknown function	other (e.g. cytoplasm)			-	1.0
AT3G57280	750	AT3G57280.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G20510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23643.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349)	226	ENV	Ch/E/IM	9.17	24.34	100.0	0.0	0.0	28.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	4.0
AT3G57560	751	AT3G57560.1	aspartate/glutamate/uridylate kinase family protein	347	THY		9.04	36.59	0.0	0.0	100.0	11.0		13.1.2.3.2 amino acid metabolism.synthesis.glutamate family.arginine.acetylglutamate kinase	chloroplast	Y	C	plastid stroma	

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AT3G57610	752	AT3G57610.1	ATPURA; adenylosuccinate synthase	490	STR		6.67	52.96	0.0	100.0	0.0	37.0		23.1.2.20 nucleotide metabolism.synthesis.purine.adenyosuccinate synthase	chloroplast	Y	C	plastid stroma	
AT3G58010	753	AT3G58010.1	Identical to Probable plastid-lipid-associated protein 9, chloroplast precursor (PAP9) [Arabidopsis Thaliana] (GB:Q9M2P7); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42130.4); similar to unknown [Populus trichocarpa] (GB:ABK96151.1)	308			5.36	34.09				3.0		26.31* misc.fibrillins	chloroplast	Y	C	plastoglobules; thylakoid-peripheral-stromal-side	
AT3G58140	754	AT3G58140.1	phenylalanyl-tRNA synthetase class IIc family protein	429	STR		5.98	49.25	0.0	100.0	0.0	96.0		29.1.20 protein.aa activation.phenylalanine-tRNA ligase	chloroplast	Y	C	mitochondria; plastid stroma	

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AT3G58160	755	AT3G58160.1	XIJ (Myosin-like protein XIJ)	1242			5.74	141.41	0.0	100.0	0.0	2.0		31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT3G58610	756	AT3G58610.1	ketol-acid reductoisomerase	591	STR		6.35	63.81	0.0	100.0	0.0	197.0		13.1.4.1.2 amino acid metabolism.synthesis.branched chain group.common.ketol-acid reductoisomerase	chloroplast	Y	C	plastid stroma	2.0
AT3G58730	757	AT3G58730.1	(VACUOLAR ATP SYNTHASE SUBUNIT D); ATPase, coupled to transmembrane movement of substances / hydrogen ion transporting ATPase, rotational mechanism	261	ENV	other	9.51	29.05	100.0	0.0	0.0	5.0	transporter ATPase	34.1.1 transport.p- and v-ATPases.H+-transporting two-sector ATPase	undefined		M	-	
AT3G59760	758	AT3G59760.1	OASC (O-ACETYLSERINE (THIOL) LYASE ISOFORM C); cysteine synthase	433	STR	Ch/E ?	8.58	46.11	6.9207842060400 1	93.07921579396	0.0	77.0	metabolism aa Cys	13.1.5.3.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	undefined	Y	C	-	

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AT3G59780	759	AT3G59780.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46311.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)	610	THY		4.55	65.33	0.0	0.0	100.0	35.0		35.2 not assigned. unknown	undefined			thylakoid	3.0
AT3G59840	760	AT3G59840.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN83312.1)	97	ENV	Ch/E/IM	4.64	10.5	100.0	0.0	0.0	7.0	redox ?	35.2 not assigned. unknown	chloroplast		C	-	
AT3G59870	761	AT3G59870.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G43945.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN60471.1)	288	STR		6.95	32.41	0.0	100.0	0.0	16.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	

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AT3G60590	762	AT3G60590.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48460.1); similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96523.1)	236	ENV	Ch/E/IM	9.6	26.27	100.0	0.0	0.0	3.0	transporter aa ?	35.2 not assigned. unknown	undefined	Y	M	-	5.0
AT3G60620	763	AT3G60620.1	phosphatidate cytidylyltransferase family protein	399	ENV	Ch/E/IM	9.3	43.25	100.0	0.0	0.0	17.0	metabolism lipid	11.3.3 lipid metabolism.Phospholipid synthesis.phosphatidate cytidylyltransferase	undefined		C	-	7.0
AT3G60750	764	AT3G60750.1	transketolase, putative	741	STR	Ch/E & Ch/S	5.93	79.96	7.9523832614301 8	91.330144116664 8	0.71747262190503 2	1702.0	metabolism carbon	1.3.8 PS.calvincyle.transketolase	chloroplast	Y	C	plastid stroma	2.0
AT3G61080	765	AT3G61080.1	fructosamine kinase family protein	326			6.51	36.47	0.0	100.0	0.0	1.0		29.4.1 protein.postranslational modification.kinase	undefined		C	plastid stroma	
AT3G61470	766	AT3G61470.1	LHCA2 (Photosystem I light harvesting complex gene 2); chlorophyll binding	257	THY	Ch/Th	6.9	27.78	5.6049825868909 2	0.0	94.395017413109 1	37.0	PS LHC	1.1.2.1 PS.lightreaction.photosystem I.LHC-I	chloroplast	Y	C	thylakoid-integral	

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AT3G61540	767	AT3G61540.1	peptidase family protein	515			6.87	57.58	0.0	100.0	0.0	3.0		29.5 protein.degradation	undefined	Y	C	-	
AT3G61770	768	AT3G61770.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G67600.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14376.1); contains InterPro domain Acid phosphatase/vanadium-dependent haloperoxidase related (InterPro:IPR003832)	284	ENV	Ch/E/IM	9.42	31.08	100.0	0.0	0.0	7.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	4.0
AT3G61870	769	AT3G61870.1	similar to unknown [Populus trichocarpa] (GB:ABK95718.1)	272	THY-ENV	Ch/E/IM	9.34	29.58	24.026713225665 7	0.0	75.973286774334 4	34.0	unknown	35.2 not assigned.unknown	undefined	Y	C	-	4.0
AT3G62030	770	AT3G62030.1	ROC4 (ROTAMASE CYP 4); peptidyl-prolyl cis-trans isomerase	260	STR-ENV	Ch	8.83	28.2	22.003370881885 8	77.996629118114 2	0.0	280.0	chaperone and protease	29.6 protein.folding	undefined	Y	C	plastid stroma	

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AT3G62410	771	AT3G62410.1	CP12-2	131			4.81	14.16	0.0	100.0	0.0	8.0		1.3 PS.calvin cyle	undefined		C	plastid stroma	
AT3G62530	772	AT3G62530.1	PBS lyase HEAT-like repeat-containing protein	221			6.14	24.5	0.0	100.0	0.0	1.0		35.1 not assigned. no ontology	undefined		M	-	
AT3G62910	773	AT3G62910.1	APG3 (ALBINO AND PALE GREEN); translation release factor	422			7.58	47.53	0.0	30.232987312572 1	69.767012687427 9	7.0		29.2.5 protein.synthesis.release	chloroplast	Y	C	plastid	
AT3G63140	774	AT3G63140.1	mRNA-binding protein, putative	406	STR-THY	Ch	8.54	43.93	20.991755898591 9	53.756258379508 4	25.251985721899 7	275.0	RNA Binding	27.3.99 RNA.regulation of transcription.unclassified	chloroplast	Y	C	plastid stroma	
AT3G63160	775	AT3G63160.1	unknown protein	69	ENV	Ch/E & Ch/Th	9.04	7.25	87.572224967263 1	0.0	12.427775032736 9	273.0	unknown	35.2 not assigned. unknown	other (e.g. cytoplasm)			envelope-outer-integral	1.0

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AT3G63170	776	AT3G63170.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26310.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22529.1); contains InterPro domain Chalcone isomerase-like (InterPro:IPR016087)	279	ENV	Ch/E/IM	6.97	30.39	91.640096077063 6	8.3599039229363 5	0.0	33.0	metabolism flavonoids ?	35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT3G63190	777	AT3G63190.1	RRF (RIBOSOME RECYCLING FACTOR, CHLOROPLAST PRECURSOR)	275	STR	Ch	9.45	30.42	7.6700627328358 2	77.5672416221649	14.7626956449993	115.0	translation stroma	29.2.9* protein.synthesis.ribosome recycling	chloroplast	Y	C	plastid stroma	
AT3G63390	778	AT3G63390.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO22605.1)	175	ENV	Ch/E ?	5.58	19.16	100.0	0.0	0.0	4.0	unknown	35.2 not assigned. unknown	other (e.g. cytoplasm)			-	

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AT3G63410	779	AT3G63410.1	APG1 (ALBINO OR PALE GREEN MUTANT 1); methyltransferase	338	ENV	Ch/E/IM	9.18	37.92	94.584939251125 1	0.0	5.4150607488749 4	412.0	metabolism vitamin and pigment	16.1.3.3 secondary metabolism.isoprenoids.tocopherol biosynthesis.MPBQ/MSBQ methyltransferase	chloroplast	Y	C	envelope -inner	1.0
AT3G63490	780	AT3G63490.1	ribosomal protein L1 family protein	346	STR-ENV	Ch/S & other	9.29	37.63	31.119071610841 3	60.562124507906 8	8.3188038812518 4	228.0	translation stroma	29.2.1.1.1.2.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L1	chloroplast	Y	C	plastid ribosome	
AT3G63520	781	AT3G63520.1	CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1)	538	ENV	Ch/E & other	6.04	60.9	100.0	0.0	0.0	4.0	metabolism hormone ABA	16.1.4.10 secondary metabolism.isoprenoids.carotenoids.carotenoid cleavage dioxygenase	undefined			cytosol	
AT4G00290	782	AT4G00290.1	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein	497	ENV	Ch/E/IM	9.06	53.88	100.0	0.0	0.0	11.0	transporter ion channel	35.1 not assigned.no ontology	undefined	Y	M	-	5.0

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AT4G00370	783	AT4G00370.1	ANTR2 (anion transporter 2); organic anion transmembrane transporter	541	ENV	Ch/E/IM	9.25	59.61	100.0	0.0	0.0	40.0	transporter Pi ?	34.7 transport.phosphate	undefined		C	envelope-inner-integral	10.0
AT4G00490	784	AT4G00490.1	BAM2/BMY9 (BETA-AMYLASE 2); beta-amylase	542	STR		4.84	62.64	0.0	100.0	0.0	17.0		2.2.2.1 major CHO metabolism.degradation.starch.starch cleavage	chloroplast	Y	C	plastid stroma	1.0
AT4G00620	785	AT4G00620.1	tetrahydrofolate dehydrogenase/cyclohydrolase, putative	360			8.57	38.74	0.0	0.0	100.0	3.0		25.5 C1-metabolism.Methylenetetrahydrofolate dehydrogenase & Methenyltetrahydrofolate cyclohydrolase	chloroplast	Y	C	plastid stroma	
AT4G00630	786	AT4G00630.1	KEA2 (K+ efflux antiporter); potassium:hydrogen antiporter	627	ENV	Ch/E	7.07	66.41	100.0	0.0	0.0	69.0	transporter K	34.15 transport.potassium	undefined		M	envelope	12.0
AT4G00640	787	AT4G00640.1	-	467	ENV	Ch/E	4.82	51.41	100.0	0.0	0.0	47.0	transporter K	-	undefined			-	1.0
AT4G00860	788	AT4G00860.1	ATOZI1 (ARABIDOPSIS THALIANA OZONE-INDUCED PROTEIN 1)	80			8.97	8.6				2.0		20 stress	secreted		S	-	

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AT4G01050	789	AT4G01050.1	hydroxyproline-rich glycoprotein family protein	466	THY		5.21	49.38	0.0	0.0	100.0	81.0		26.23 misc.rhodanese	chloroplast	Y	C	thylakoid	2.0
AT4G01150	790	AT4G01150.1	Identical to Uncharacterized protein At4g01150, chloroplast precursor [Arabidopsis Thaliana] (GB:O04616;GB:Q38835); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G38100.1); similar to unknown [Populus trichocarpa] (GB:ABK95729.1)	164	THY	Ch/E & Ch/Th	9.21	17.69	5.6049825868909 2	0.0	94.395017413109 1	109.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	thylakoid-integral	2.0
AT4G01310	791	AT4G01310.1	ribosomal protein L5 family protein	262	STR-ENV	Ch/S	10.0	28.34	26.724540758060 4	64.702598862440 1	8.572860379499 5 3	352.0	translation stroma	29.2.1.1.1.2.5 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L5	chloroplast	Y	C	plastid ribosome	

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AT4G01690	792	AT4G01690.1	PPOX (PROTOPORPHYRINOGEN OXIDASE); protoporphyrinogen oxidase	537	ENV-THY	Ch/E/IM	9.13	57.69	62.719608146719 8	0.0	37.280391853280 2	69.0	metabolism vitamin and pigment	19.9 tetrapyrrole synthesis.protoporphyrin IX oxidase	undefined	Y	M	plastid	1.0
AT4G01800	793	AT4G01800.1	preprotein translocase secA subunit, putative	1022	STR	Ch/S & Ch/Th	6.07	115.18	9.820595 8413009 3	87.029093822100 5	3.150310 3365985 4	105.0	protein targeting	29.3.3 protein.targeting.chloroplast	undefined	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT4G01883	794	AT4G01883.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G02475.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40177.1); contains InterPro domain Streptomyces cyclase/dehydrase (InterPro:IPR005031)	224			9.86	25.28	0.0	100.0	0.0	2.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid	
AT4G01900	795	AT4G01900.1	GLB1 (glutamine synthetase B1)	196	THY		9.17	21.27	0.0	8.496890 2220282 1	91.50310 9777971 8	15.0		30.1.1 signalling.in sugar and nutrient physiology	undefined	Y	C	plastid stroma	

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AT4G02510	796	AT4G02510.1	TOC159 (PLASMID PROTEIN IMPORT 2)	1503	ENV	Ch/E & other	4.42	160.82	98.746314951872 4	0.0	1.2536850481276 2	389.0	protein targeting Toc	29.3.3 protein.targeting.chloroplast	undefined			envelope-outer	
AT4G02520	797	AT4G02520.1	ATGSTF2 (Arabidopsis thaliana Glutathione S-transferase (class phi) 2); glutathione transferase	212	STR		5.92	24.12	0.0	100.0	0.0	37.0		26.9 misc.glutathione S transferases	undefined			not plastid	
AT4G02530	798	AT4G02530.1	chloroplast thylakoid lumen protein	216	THY-ENV	Ch/Th/Lum	8.54	23.66	31.730319590689 1	2.8355372321133 2	65.434143177197 6	41.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT4G16155	854	AT4G16155.1	dihydrolipoamide dehydrogenase 2, plastidic / lipoamide dehydrogenase 2 (PTLPD2)	567	ENV-STR	Ch/E/IM	7.29	60.14	52.099296955045 8	40.738105041186 3	7.1625980037678 9	73.0	metabolism lipid	11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	other (e.g. cytoplasm)	Y	C	plastid	

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AT4G02620	799	AT4G02620.1	(VACUOLAR ATPASE SUBUNIT F); hydrogen ion transporting ATP synthase, rotational mechanism / hydrogen ion transporting ATPase, rotational mechanism	128	ENV	other	6.07	14.26	100.0	0.0	0.0	3.0	transporter ATPase	34.1.1 transport.p- and v-ATPases.H+-transporting two-sector ATPase	undefined			vacuole	
AT4G02725	800	AT4G02725.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO22536.1)	165			8.88	18.79	0.0	0.0	100.0	3.0		35.2 not assigned.unknown	chloroplast	Y	C	-	
AT4G02770	801	AT4G02770.1	PSAD-1 (photosystem I subunit D-1)	208	THY-ENV	Ch/Th	9.78	22.59	21.524762185732 9	0.16420389603254 5	78.3110339182346	422.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT4G02990	802	AT4G02990.1	mitochondrial transcription termination factor family protein / mTERF family protein	541			6.33	61.55	0.0	100.0	0.0	2.0		27.3.99 RNA.regulation of transcription.unclassified	undefined	Y	M	plastid	

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AT4G03080	803	AT4G03080.1	kelch repeat-containing serine/threonine phosphoesterase family protein	881			5.91	96.14	0.0	24.528678553158 6	75.471321446841 4	2.0		29.4 protein.postranslational modification	other (e.g. cytoplasm)			-	
AT4G03200	804	AT4G03200.1	catalytic	818			5.92	91.83	0.0	100.0	0.0	3.0		35.2 not assigned. unknown	undefined	Y	C	plastid	
AT4G03205	805	AT4G03205.1	HEMF2; coproporphyrinogen oxidase	233	STR		7.09	26.13	0.0	100.0	0.0	18.0		19.8 tetrapyrrole synthesis.coproporphyrinogen III oxidase	chloroplast	Y	C	-	
AT4G03280	806	AT4G03280.1	PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C)	229	THY	Ch & other	8.8	24.36	6.3467244049239 7	0.0	93.653275595076	84.0	PS b6-F	1.1.3 PS.lightreaction.cytochrome b6/f	undefined	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT4G03430	807	AT4G03430.1	EMB2770/STA1 (STABILIZED1); RNA splicing factor, transesterification mechanism	1029			6.85	115.57				6.0		27.1.1 RNA.processing.splicing	undefined	Y		-	
AT4G03520	808	AT4G03520.1	ATHM2 (Arabidopsis thioredoxin M-type 2); thiol-disulfide exchange intermediate	186	STR		9.35	20.31	0.0	100.0	0.0	52.0		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	

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AT4G04020	809	AT4G04020.1	FIB (FIBRILLIN); structural molecule	318	THY		5.44	34.94	0.0	0.0	100.0	30.0		26.31* misc.fibrillins	chloroplast	Y	C	plastoglobules; thylakoid-peripheral-stromal-side	
AT4G04350	810	AT4G04350.1	EMB2369 (EMBRYO DEFECTIVE 2369); ATP binding / aminoacyl-tRNA ligase	973	STR		5.91	111.03	0.0	100.0	0.0	21.0		29.1.4 protein.aa activation.leucine-tRNA ligase	chloroplast	Y	C	plastid stroma	
AT4G04640	811	AT4G04640.1	ATPC1 (ATP synthase gamma chain 1)	373	THY-ENV	Ch/Th	8.13	40.91	16.789376931141 5	1.9869632887844 3	81.223659780074	588.0	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT4G04770	812	AT4G04770.1	ATABC1 (ARABIDOPSIS THALIANA NUCLEOSOME ASSEMBLY PROTEIN 1)	557	STR		6.44	61.86	0.0	100.0	0.0	12.0		14 S-assimilation	chloroplast	Y	C	plastid	
AT4G05180	813	AT4G05180.1	PSBQ/PSBQ-2/PSII-Q (PHOTOSYSTEM II SUBUNIT Q-2); calcium ion binding	230	THY	Ch/Th/Lum	9.72	24.64	4.4980077048211 1	8.2066505528999 4	87.295341742279	334.0	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined	Y	C	thylakoid-peripheral-lumenal-side	
AT4G05390	814	AT4G05390.1	ATRFNR1 (ROOT FNR 1); oxidoreductase	378			8.77	42.39	0.0	100.0	0.0	8.0		7.3 OPP.electron transfer	chloroplast	Y	C	-	

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AT4G08390	815	AT4G08390.1	SAPX; L-ascorbate peroxidase	372	STR		8.3	40.4	0.0	100.0	0.0	37.0		21.2.1 redox.ascorbate and glutathione.ascorbate	chloroplast	Y	C	mitochondria; plastid stroma	
AT4G09000	816	AT4G09000.1	GRF1 (GENERAL REGULATORY FACTOR 1); protein phosphorylated amino acid binding	267	STR		4.68	29.93	0.0	100.0	0.0	13.0		30.7 signalling.14-3-3 proteins	undefined			-	
AT4G09010	817	AT4G09010.1	APX4 (ASCORBATE PEROXIDASE 4); peroxidase	349	THY	Lum	8.58	37.93	0.0	0.0	100.0	85.0		21.2.1 redox.ascorbate and glutathione.ascorbate	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT4G09020	818	AT4G09020.1	ATISA3/ISA3 (ISOAMYLASE 3); alpha-amylase	764	STR		5.65	86.32	0.0	100.0	0.0	15.0		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	chloroplast	Y	C	plastid stroma	
AT4G09040	819	AT4G09040.1	RNA recognition motif (RRM)-containing protein	304	STR		7.11	34.03	0.0	100.0	0.0	11.0		27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	

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AT4G09320	820	AT4G09320.1	NDPK1 (nucleoside diphosphate kinase 1); ATP binding / nucleoside diphosphate kinase	169	ENV	Ch/S & other	8.42	18.81	86.476285785767 9	13.523714214232 1	0.0	3.0	metabolism nucleotide	23.4.10 nucleotide metabolism.phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase	undefined			-	
AT4G09430	821	AT4G09430.1	disease resistance protein (TIR-NBS-LRR class), putative	1039			7.55	118.37	0.0	100.0	0.0	1.0		20.1.7 stress.biotic.PR-proteins	undefined			-	
AT4G09650	822	AT4G09650.1	ATP synthase delta chain, chloroplast, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative	234	THY-ENV	Ch	9.04	25.66	20.333829741248	4.4029858737041 7	75.263184385047 9	175.0	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	

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AT4G10000	823	AT4G10000.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G03880.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16313.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredoxin fold	333			8.94	37.05	0.0	0.0	100.0	4.0		21.4 redox.glutaredoxins	chloroplast	Y	C	-	

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AT4G10300	824	AT4G10300.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04300.1); similar to unknown [Populus trichocarpa] (GB:ABK95374.1); contains InterPro domain RmlC-like jelly roll fold (InterPro:IPR014710); contains InterPro domain Protein of unknown funct	134			8.89	14.93	0.0	100.0	0.0	5.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid	
AT4G10340	825	AT4G10340.1	LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	280	THY	Ch/Th	5.99	30.15	1.7666933504786 1	0.0	98.233306649521 4	783.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0
AT4G10750	826	AT4G10750.1	HpcH/HpaI aldolase family protein	358			5.69	38.4	0.0	100.0	0.0	6.0		35.1 not assigned. no ontology	chloroplast	Y	C	-	

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AT4G11150	827	AT4G11150.1	TUF (VACUOLAR ATP SYNTHASE SUBUNIT E1)	230	ENV	other	6.04	26.06	100.0	0.0	0.0	6.0	transporter ATPase	34.1.1 transport.p- and v-ATPases.H+-transporting two-sector ATPase	undefined			vacuole	
AT4G11175	828	AT4G11175.1	translation initiation factor IF-1, chloroplast, putative	141			10.15	15.73	0.0	24.528678553158 6	75.471321446841 4	4.0		29.2.3 protein.synthesis.initiation	undefined	Y	M	plastid stroma	
AT4G11960	829	AT4G11960.1	PGRL1B (PGR5-LIKE B)	313			5.05	34.91	0.0	0.0	100.0	3.0		1.1.40 PS.lightreaction.cyclic electron flow-chlororespiration	chloroplast	Y	C	thylakoid-integral	2.0
AT4G11980	830	AT4G11980.1	ATNUDT14 (Arabidopsis thaliana Nudix hydrolase homolog 14); hydrolase	309	STR		6.98	34.25	0.0	100.0	0.0	19.0		26.13 misc.acid and other phosphatases	undefined	Y	M	plastid	
AT4G12060	831	AT4G12060.1	Clp amino terminal domain-containing protein	241	ENV-STR	Ch/E & Ch/S	8.85	26.56	56.118865710137 3	43.881134289862 7	0.0	41.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT4G12770	832	AT4G12770.1	heat shock protein binding	891			6.58	100.3				2.0		31.4 cell.vesicle transport	undefined	Y		-	

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AT4G12800	833	AT4G12800.1	PSAL (photosystem I subunit L)	219	THY	Ch/Th	9.85	23.05	4.8205818087446	0.3350548400404 13	94.844363351214 9	248.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-integral	2.0
AT4G12830	834	AT4G12830.1	hydrolase, alpha/beta fold family protein	393	ENV	Ch/E/IM	8.59	43.76	100.0	0.0	0.0	1.0	hydrolase ?	35.1 not assigned. no ontology	undefined	Y	M	-	
AT4G13010	835	AT4G13010.1	oxidoreductase, zinc-binding dehydrogenase family protein	329	ENV	Ch/E & Ch/Th	9.04	34.43	93.971077487858 7	0.0	6.0289225121413 4	16.0	redox ?	26.7 misc.oxidases - copper, flavone etc.	undefined			envelope-inner-peripheral-stromal-side	
AT4G13140	836	AT4G13140.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO46123.1)	137	ENV	Ch/E ?	9.38	14.79	100.0	0.0	0.0	7.0	unknown	35.2 not assigned. unknown	undefined			-	2.0
AT4G13150	837	AT4G13150.1	unknown protein	119	ENV	Ch/E ?	9.16	12.77	100.0	0.0	0.0	2.0	unknown	35.2 not assigned. unknown	undefined			-	

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AT4G13200	838	AT4G13200.1	Identical to Uncharacterized protein At4g13200, chloroplast precursor [Arabidopsis Thaliana] (GB:Q8LDV3;GB:Q9SVQ7); similar to unknown [Picea sitchensis] (GB:ABK25970.1); similar to unknown [Picea sitchensis] (GB:ABK22042.1)	185			5.26	20.43	0.0	0.0	100.0	5.0		35.2 not assigned. unknown	chloroplast	Y	C	plastoglobules	
AT4G13430	839	AT4G13430.1	aconitase family protein / aconitate hydratase family protein	509	STR		8.07	55.01	0.0	100.0	0.0	58.0		13.1.4.4 amino acid metabolism.synthesis.branched chain group.leucine specific	chloroplast	Y	C	plastid	

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AT4G13500	840	AT4G13500.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G05310.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41162.1)	125	THY	Ch/E ?	9.06	13.81	5.1854294154885	0.0	94.814570584511 5	24.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	1.0
AT4G13590	841	AT4G13590.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G64150.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71558.1); contains InterPro domain Protein of unknown function UPF0016; (InterPro:IPR001727)	359	ENV	Ch/E/IM	8.82	37.93	100.0	0.0	0.0	5.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	6.0

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AT4G13670	842	AT4G13670.1	PTAC5 (PLASTID TRANSCRIPTIONALLY ACTIVE5); heat shock protein binding / unfolded protein binding	387	ENV-THY	Ch/E & Ch/Th	4.84	44.02	83.153048662390 9	0.0	16.846951337609 1	23.0	unknown	26.29* misc.DnaJ domain with unknown function	chloroplast	Y	C	-	
AT4G13940	843	AT4G13940.1	HOG1 (HOMOLOGY-DEPENDENT GENE SILENCING 1); adenosyl homocysteinase	485			5.66	53.37	0.0	100.0	0.0	3.0		13.2.3.4 amino acid metabolism.degradation.aspartate family.methionine	other (e.g. cytoplasm)			-	
AT4G14070	844	AT4G14070.1	AAE15 (ACYL-ACTIVATING ENZYME 15); long-chain-fatty-acid-[acyl-carrier-protein] ligase	727	ENV	Ch/E/IM	8.89	81.46	99.235995402807 6	0.0	0.764004597192417	126.0	metabolism lipid	11.1.8 lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	chloroplast	Y	C	envelope	
AT4G14210	845	AT4G14210.1	PDS3 (PHYTOENE DESATURASE)	566	ENV-THY	Ch/E/IM	6.07	62.96	84.383280311822 6	0.0	15.616719688177 4	33.0	metabolism vitamin and pigment	16.1.4.2 secondary metabolism.isoprenoids.carotenoids.phytoene dehydrogenase	undefined	Y	C	-	

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AT4G14880	846	AT4G14880.1	OASA1 (O-ACETYL SERINE (THIOL) LYASE (OAS-TL) ISOFORM A1)	322	STR		5.9	33.8	0.0	100.0	0.0	15.0		13.1.5.3.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	undefined			-	
AT4G14890	847	AT4G14890.1	ferredoxin family protein	154			4.74	16.73	0.0	100.0	0.0	5.0		26.30 misc.other Ferredoxins and Rieske domain	chloroplast	Y	C	-	
AT4G15110	848	AT4G15110.1	CYP97B3 (cytochrome P450, family 97, subfamily B, polypeptide 3); oxygen binding	580	ENV	Ch/E & Ch/S	6.39	65.17	100.0	0.0	0.0	11.0	cytochrome P450	26.10 misc.cytochrome P450	undefined	Y	M	-	
AT4G15510	849	AT4G15510.1	photosystem II reaction center PsbP family protein	287		Lum	8.92	32.26	0.0	0.0	100.0	4.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT4G15530	850	AT4G15530.1	PPDK (PYRUVATE ORTHOPHOSPHATE DIKINASE); kinase/ pyruvate, phosphate dikinase	956	STR		5.82	104.2	0.0	100.0	0.0	10.0		4.4 glycolysis.PPFK	undefined			plastid stroma	

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AT4G15560	851	AT4G15560.1	CLA1 (CLOROPLASTOS ALTERADOS 1)	717			7.04	76.83	0.0	100.0	0.0	4.0		16.1.1.1 secondary metabolism.isoprenoids.non-mevalonate pathway.DXS	chloroplast	Y	C	plastid stroma	
AT4G15820	852	AT4G15820.1	wound-responsive protein-related	460	ENV	CH/E/IM	5.15	51.21	100.0	0.0	0.0	4.0	unknown	20.2.4 stress.abiotic.touch/wounding	undefined	Y	M	-	1.0
AT4G16060	853	AT4G16060.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO44835.1)	289			5.31	27.02	0.0	100.0	0.0	7.0		35.2 not assigned.unknown	chloroplast	Y		plastid	
AT4G16390	855	AT4G16390.1	chloroplastic RNA-binding protein P67, putative	688	STR		5.82	76.63	0.0	100.0	0.0	15.0		27.4 RNA.RNA binding	chloroplast		C	plastid stroma	
AT4G17040	856	AT4G17040.1	ATP-dependent Clp protease proteolytic subunit, putative	305	STR-ENV	Ch/E & Ch/S	9.33	33.44	41.717914398547 4	58.282085601452 6	0.0	96.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT4G17170	857	AT4G17170.1	AT-RAB2 (Arabidopsis Rab GTPase homolog B1c); GTP binding	211	ENV	Ch/E ?	6.95	23.16	100.0	0.0	0.0	6.0	signalling / SNARE effector	30.5 signalling.G-proteins	undefined			-	
AT4G17300	858	AT4G17300.1	NS1 (OVULE ABORTION 8)	567	STR		5.79	63.69	0.0	100.0	0.0	15.0		29.1.22 protein.aa activation.asparagine-tRNA ligase	chloroplast	Y	C	mitochondria; plastid stroma	

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AT4G17530	859	AT4G17530.1	RAB1C; GTP binding	202	ENV	Ch/E ?	5.27	22.31	100.0	0.0	0.0	5.0	signalling / SNARE effector	30.5 signalling.G-proteins	secreted		S	-	
AT4G17540	860	AT4G17540.1	similar to hypothetical protein OsI_033497 [Oryza sativa (indica cultivar-group)] (GB:EAY79538.1); similar to Os10g0563400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001065401.1)	294	ENV	Ch/E ?	9.56	31.75	100.0	0.0	0.0	2.0	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	2.0
AT4G17560	861	AT4G17560.1	ribosomal protein L19 family protein	225	STR-ENV	Ch/S	10.03	25.51	43.221829853702 6	56.778170146297 4	0.0	35.0	translation stroma	29.2.1.1.1.2.19 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L19	chloroplast	Y	C	plastid ribosome	
AT4G17600	862	AT4G17600.1	LIL3:1; transcription factor	262			4.94	29.4	0.0	0.0	100.0	9.0		1.1.8* light stress chlorophyll binding	chloroplast	Y	C	thylakoid-integral	2.0
AT4G17740	863	AT4G17740.1	C-terminal processing protease, putative	515		Lum	8.97	55.76	0.0	0.0	100.0	3.0		29.9* protein.processing	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	

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AT4G18370	864	AT4G18370.1	DEG5/DEGP5/HHOA (DEGP PROTEASE 5); serine-type peptidase/ trypsin	323		Lum	5.19	34.92				2.0		29.5.5 protein.degradation.serine protease	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT4G18440	865	AT4G18440.1	adenylosuccinate lyase, putative / adenylosuccinase, putative	536	STR		5.88	59.75	0.0	100.0	0.0	147.0		23.1.2.8 nucleotide metabolism.synthesis.purine.SAICAR lyase	chloroplast	Y	C	plastid stroma	
AT4G18480	866	AT4G18480.1	CHLI1 (CHLORINA 42); magnesium chelatase	424	STR	Ch/S & other	6.08	46.27	2.2968917079809 5	97.703108292019 1	0.0	342.0	metabolism vitamin and pigment	19.10 tetrapyrrole synthesis.magnesium chelatase	chloroplast	Y	C	plastid stroma	
AT4G18810	867	AT4G18810.1	binding / catalytic/ transcription repressor	596	STR	Ch/E & other	8.16	65.46	15.083160860783 5	84.916839139216 5	0.0	38.0	protein targeting tic ?	20.2.99 stress.abiotic.unspecified	chloroplast	Y	C	plastid stroma	
AT4G19100	868	AT4G19100.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G52780.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN79943.1)	214			8.69	24.21	0.0	0.0	100.0	2.0		35.2 not assigned. unknown	chloroplast	Y	C	-	

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AT4G19390	869	AT4G19390.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13720.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63752.1); contains InterPro domain Uncharacterised conserved protein UCP022348 (InterPro:IPR016804); contains InterPro do	273	ENV	Ch/E/IM	9.29	30.04	100.0	0.0	0.0	17.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	4.0
AT4G19710	870	AT4G19710.2	AK-HSDH/AK-HSDH II; aspartate kinase/homoserine dehydrogenase	859	STR		6.35	94.42	0.0	100.0	0.0	89.0		13.1.3.6.1.10 amino acid metabolism.synthesis.aspartate family.misc.homoserine.bifunctional aspartate kinase/homoserine dehydrogenase	chloroplast	Y	C	plastid	

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AT4G20260	871	AT4G20260.1	DREPP plasma membrane polypeptide family protein	225	ENV	Ch/E ?	4.99	24.58	93.501193686343 9	6.4988063136561 2	0.0	11.0	stress ?	35.1 not assigned. no ontology	undefined			plasma membrane	
AT4G20360	872	AT4G20360.1	AtRABE1b/AtRab8D (Arabidopsis Rab GTPase homolog E1b); translation elongation factor	476	STR-THY	Ch & other	5.83	51.63	8.1987994016928 5	72.712050851499 8	19.0891497468073	1376.0	translation stroma / signalling / SNARE effector	29.2.4 protein.synthesis. elongation	chloroplast	Y	C	plastid stroma	
AT4G20850	873	AT4G20850.1	TPP2 (TRIPEPTIDYL PEPTIDASE II); subtilase	1380			5.76	152.36	0.0	100.0	0.0	6.0		29.5.1 protein.degradation.subtilases	chloroplast	Y	C	plastid stroma	
AT4G20960	874	AT4G20960.1	cytidine/deoxycytidylate deaminase family protein	426	STR		6.04	46.67	0.0	100.0	0.0	10.0		23.5.3 nucleotide metabolism.deoxynucleotide metabolism.cytosine deaminase	chloroplast	Y	C	plastid	
AT4G21210	875	AT4G21210.1	phosphoprotein phosphatase/ protein kinase	403			6.93	43.68	0.0	100.0	0.0	5.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT4G21280	876	AT4G21280.1	PSBQ/PSBQ-1/PSBQA; calcium ion binding	223	THY	Ch/Th/Lum	9.64	23.79	5.3523643250583 2	0.0	94.647635674941 7	314.0	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	

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AT4G21445	877	AT4G21445.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO42770.1)	154			6.59	17.61	0.0	100.0	0.0	7.0		35.2 not assigned. unknown	undefined	Y	C	plastid stroma	
AT4G21670	878	AT4G21670.1	CPL1 (FIERY 2); double-stranded RNA binding	967			5.81	108.42	0.0	100.0	0.0	9.0		27.4 RNA.RNA binding	other (e.g. cytoplasm)			-	2.0
AT4G22130	879	AT4G22130.1	SRF8 (STRUBBELIG-RECEPTOR FAMILY 8); kinase	703			6.92	76.08	0.0	100.0	0.0	6.0		29.4.1.57 protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII; 30.2.5 signalling.receptor kinases.leucine rich repeat V	secreted		S	-	
AT4G22240	880	AT4G22240.1	plastid-lipid associated protein PAP, putative	310	THY	Ch	5.67	33.65	0.0	0.0	100.0	17.0	PAP_fibrillin	26.31* misc.fibrillins	chloroplast	Y	C	plastoglobules; thylakoid-peripheral-stromal-side	
AT4G22570	881	AT4G22570.1	APT3 (ADENINE PHOSPHORIBOSYL TRANSFERASE 3); adenine phosphoribosyltransferase	183			5.83	20.35	0.0	100.0	0.0	5.0		23.3.1.1 nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	other (e.g. cytoplasm)			cytosol	

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AT4G22890	882	AT4G22890.1	PGR5-LIKE A	324	THY		5.2	35.72	0.0	0.8707476364377726	99.129252363562 3	49.0		1.1.40 PS.lightreaction.cyclic electron flow-chlororespiration	chloroplast	Y	C	thylakoid-integral	2.0
AT4G22930	883	AT4G22930.1	PYR4 (PYRIMIDIN 4); dihydroorotase	377			8.63	41.95	0.0	100.0	0.0	7.0		23.1.1.3 nucleotide metabolism.synthesis.pyrimidine.dihydroorotase	undefined			plastid	
AT4G23100	884	AT4G23100.1	RML1 (ROOT MERISTEMLESS 1); glutamate-cysteine ligase	522	STR		6.16	58.56	0.0	100.0	0.0	75.0		21.2.2 redox.ascorbate and glutathione.glutathione	undefined	Y	C	plastid stroma	
AT4G23430	885	AT4G23430.1	short-chain dehydrogenase/reductase (SDR) family protein	320	ENV	Ch/E/IM	8.95	34.49	100.0	0.0	0.0	12.0	protein targeting Tic	26.22 misc.short chain dehydrogenase/reductase (SDR)	undefined			-	
AT4G23890	886	AT4G23890.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO69542.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN73381.1)	250	THY		8.31	27.72	0.0	0.0	100.0	13.0		35.2 not assigned. unknown	undefined	Y	C	thylakoid	

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AT4G23940	887	AT4G23940.1	FtsH protease, putative	946	ENV	Ch/E/IM	7.64	105.54	99.595444879124 2	0.40455512087578 4	0.0	78.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	-	3.0
AT4G24280	888	AT4G24280.1	CPHSC70-1 (chloroplast heat shock protein 70-1); ATP binding / unfolded protein binding	718	STR	Ch & other	5.06	76.5	8.791234967576	90.738747414393 3	0.4700176180306 74	818.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT4G24460	889	AT4G24460.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G19380.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61583.1); contains domain Multidrug resistance efflux transporter EmrE (SSF103481)	431	ENV	Ch/E/IM	9.93	46.68	100.0	0.0	0.0	5.0	transporter ?	35.2 not assigned.unknown	chloroplast	Y	C	-	10.0
AT4G24620	890	AT4G24620.1	PGI1 (CHLOROPLASTIC PHOSPHOGLUCOSE ISOMERASE)	613	STR	Ch/S	5.46	67.04	4.6881818104312 2	95.311818189568 8	0.0	99.0	metabolism carbon	4.3 glycolysis.G6PIsomerase	chloroplast	Y	C	plastid stroma	

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AT4G24770	891	AT4G24770.1	RBP31 (31-KDA RNA BINDING PROTEIN); RNA binding / poly(U) binding	329	STR-ENV	Ch & other	4.58	35.78	16.410315241327 9	83.589684758672 1	0.0	164.0	RNA Binding	27.1.5* RNA.editing	chloroplast	Y	C	plastid stroma	
AT4G24830	892	AT4G24830.1	arginosuccinate synthase family	494	STR		6.25	53.84	0.0	100.0	0.0	62.0		13.1.2.3.22 amino acid metabolism.synthesis.glutamate family.arginine.arginosuccinate synthase	chloroplast	Y	C	plastid stroma	
AT4G24930	893	AT4G24930.1	thylakoid lumenal 17.9 kDa protein, chloroplast	225		Lum	6.39	24.69	0.0	0.0	100.0	3.0		35.2 not assigned. unknown	undefined	Y	C	thylakoid-peripheral-lumenal-side	
AT4G25050	894	AT4G25050.1	ACP4 (ACYL CARRIER PROTEIN 4)	137	STR-ENV	Ch/E/IM	4.73	14.54	32.970405234885 8	67.029594765114 2	0.0	20.0	metabolism lipid	11.1.12 lipid metabolism.FA synthesis and FA elongation.ACP protein	chloroplast	Y	C	plastid stroma	
AT4G25080	895	AT4G25080.1	CHLM (MAGNESIUM-PROTOPORPHYRIN IX METHYL TRANSFERASE); magnesium protoporphyrin IX methyltransferase	312	ENV-THY	Ch/E/IM	7.68	33.79	64.432171244050 7	1.119590522790 74	34.448238233158 5	44.0	metabolism vitamin and pigment	19.11 tetrapyrrole synthesis.magnesium protoporphyrin IX methyltransferase	chloroplast	Y	C	plastid	

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AT4G25100	896	AT4G25100.1	FSD1 (FE SUPEROXIDE DISMUTASE 1); iron superoxide dismutase	212	STR		6.05	23.79	0.0	100.0	0.0	53.0		21.6 redox.dismutases and catalases	undefined			cytosol; plastid stroma	
AT4G25130	897	AT4G25130.1	peptide methionine sulfoxide reductase, putative	258	STR-ENV	Ch	8.95	28.64	41.097252328696 3	53.252707945357 7	5.650039 7259459 9	43.0	protein modification	29.11* protein.methione sulfoxide reductases	chloroplast	Y	C	plastid stroma	
AT4G25370	898	AT4G25370.1	Clp amino terminal domain-containing protein	238	ENV-STR	Ch	9.24	26.05	56.951903755726 7	43.048096244273 3	0.0	48.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT4G25450	899	AT4G25450.1	ATNAP8 (Arabidopsis thaliana non-intrinsic ABC protein 8); ATPase, coupled to transmembrane movement of substances	714	ENV	Ch/E/IM	9.12	77.92	99.405813660601 2	0.0	0.594186 3393988 35	162.0	transporter ABC	34.8 transport.metabolite transporters at the envelope membrane; 34.16 transport.ABC transporters and multidrug resistance systems	undefined	Y	M	envelope-inner-integral; envelope	5.0
AT4G25650	900	AT4G25650.1	ACD1-LIKE; electron carrier	536	ENV	Ch/E/IM	8.9	61.26	100.0	0.0	0.0	55.0	protein targeting Tic ?	26.30 misc.other Ferredoxins and Rieske domain	chloroplast	Y	C	-	2.0
AT4G25900	901	AT4G25900.1	aldose 1-epimerase family protein	318			9.65	36.25	0.0	0.0	100.0	2.0		3.5 minor CHO metabolism.others	secreted		S	-	

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AT4G25910	902	AT4G25910.1	NFU3 (NFU domain protein 3)	236	STR		6.45	25.65	0.0	100.0	0.0	11.0		29.8.1* protein assembly and cofactor ligation.Fe-S assembly	chloroplast	Y	C	plastid	
AT4G26300	903	AT4G26300.1	EMB1027 (EMBRYO DEFECTIVE 1027); ATP binding / arginine-tRNA ligase	642	STR		6.73	72.38	0.0	100.0	0.0	34.0		29.1.19 protein.aa activation.arginine-tRNA ligase	undefined			plastid stroma	
AT4G26530	904	AT4G26530.1	fructose-bisphosphate aldolase, putative	358			5.64	38.29	0.0	100.0	0.0	2.0		4.7 glycolysis.aldolase	undefined			cytosol	
AT4G26670	905	AT4G26670.1	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	210	ENV	Ch/E/OM	7.62	21.81	100.0	0.0	0.0	4.0	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane	other (e.g. cytoplasm)			envelope-inner-integral	2.0
AT4G26900	906	AT4G26900.1	AT-HF (ARABIDOPSIS THALIANA HISF PROTEIN)	592	STR		6.3	64.19	0.0	100.0	0.0	46.0		13.1.7.10 amino acid metabolism.synthesis.histidine.Imidazole glycerol phosphate synthase	chloroplast	Y	C	plastid stroma	

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AT4G27070	907	AT4G27070.1	TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT); tryptophan synthase	475	STR-ENV	Ch/E ?	6.2	51.6	22.519983469659	77.480016530341	0.0	32.0	metabolism amino acid Trp	13.1.6.5.5 amino acid metabolism.synthesis.aromatic aa.tryptophan.tryptophan synthase	chloroplast	Y	C	-	
AT4G27440	908	AT4G27440.1	PORB (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B); oxidoreductase/ protochlorophyllide reductase	401	ENV-THY	Ch/E & Ch/Th	9.22	43.36	58.141590856085 4	6.9232641189619 6	34.935145024952 7	546.0	metabolism vitamin and pigment	19.14 tetrapyrrole synthesis.protochlorophyllide reductase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT4G27700	909	AT4G27700.1	rhodanese-like domain-containing protein	224	ENV-THY	Ch/E & Ch/Th	8.78	24.87	70.042002003111 5	0.0	29.957997996888 4	17.0	unknown	26.23 misc.rhodanese	chloroplast	Y	C	thylakoid	
AT4G27990	910	AT4G27990.1	YGGT family protein	218	ENV	Ch/E/IM	11.28	23.7	96.641464484094 9	3.3585355159050 7	0.0	11.0	cytochrome biogenesis ?	35.1 not assigned.no ontology	chloroplast	Y	C	-	3.0
AT4G28025	911	AT4G28025.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO66511.1); contains domain Chlorophyll a-b binding protein (SSF103511)	157	THY		10.59	16.95	0.0	0.0	100.0	12.0		35.2 not assigned.unknown	chloroplast	Y	C	-	1.0

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AT4G28210	912	AT4G28210.1	EMB1923 (EMBRYO DEFECTIVE 1923)	348	ENV	Ch/E/IM	9.76	38.34	100.0	0.0	0.0	6.0	transporter aa ?	35.2 not assigned. unknown	chloroplast	Y	C	-	7.0
AT4G28440	913	AT4G28440.1	DNA-binding protein-related	153	ENV	Ch/E/IM	9.46	16.45	100.0	0.0	0.0	3.0	DNA binding ?	28.99 DNA.unspecified	undefined	Y	C	-	
AT4G28660	914	AT4G28660.1	PSB28 (PHOTOSYSTEM II REACTION CENTER PSB28 PROTEIN)	183			9.46	20.19	0.0	56.522239153560 8	43.477760846439 2	7.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT4G28706	915	AT4G28706.1	pfkB-type carbohydrate kinase family protein	401			5.93	43.08	0.0	100.0	0.0	5.0		3.5 minor CHO metabolism.others	undefined	Y	C	plastid stroma	
AT4G28750	916	AT4G28750.1	PSAE-1 (PSA E1 KNOCKOUT); catalytic	143	THY-ENV	Ch/Th	9.92	14.96	23.288901309006 8	1.324388079574 3 1	75.386710611418 8	225.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT4G29060	917	AT4G29060.1	EMB2726 (EMBRYO DEFECTIVE 2726); translation elongation factor	953	STR	Ch/E & Ch/S	4.95	103.78	3.714705838401 1 1	94.497855335699 5	1.787438258993 5	719.0	translation stroma	29.2.4 protein.synthesis.elongation	chloroplast	Y	C	plastid ribosome	

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AT4G29130	918	AT4G29130.1	ATHXK1 (GLUCOSE INSENSITIVE 2); ATP binding / hexokinase	496	ENV	Ch/E & other	5.75	53.7	100.0	0.0	0.0	4.0	metabolism carbon	2.2.1.4 major CHO metabolism.degradation.sucrose.hexokinase	secreted		S	-	
AT4G29590	919	AT4G29590.1	methyltransferase	317			6.97	35.37	0.0	100.0	0.0	7.0		29.4 protein.postranslational modification	chloroplast	Y	C	plastid	
AT4G29670	920	AT4G29670.1	thioredoxin family protein	235			9.05	25.84	0.0	100.0	0.0	5.0		21.1 redox.thioredoxin	undefined	Y	C	plastid stroma	
AT4G29840	921	AT4G29840.1	MTO2 (METHIONINE OVER-ACCUMULATOR); threonine synthase	526	STR		7.11	57.77	0.0	100.0	0.0	125.0		13.1.3.2.1 amino acid metabolism.synthesis.aspartate family.threonine.threonine synthase	chloroplast	Y	C	plastid stroma	
AT4G30580	922	AT4G30580.1	ATS2 (EMBRYO DEFECTIVE 1995); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	356	ENV	Ch/E/IM	9.87	39.39	100.0	0.0	0.0	28.0	metabolism lipid	11.10 lipid metabolism.glycolipid synthesis	undefined	Y	C	envelope-inner-integral	3.0

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AT4G30620	923	AT4G30620.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24020.1); similar to unknown [Picea sitchensis] (GB:ABK26000.1); similar to Os02g0180200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046090.1); contains InterPro domain Conserved hypo	180	STR-ENV	Ch/E ?	9.18	19.58	16.370303880486 6	83.629696119513 4	0.0	63.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	
AT4G30690	924	AT4G30690.1	translation initiation factor 3 (IF-3) family protein	281			9.54	31.82	0.0	24.528678553158 6	75.471321446841 4	5.0		29.2.3 protein.synthesis.initiation	chloroplast	Y	C	plastid stroma	
AT4G30910	925	AT4G30910.1	cytosol aminopeptidase family protein	581	STR		6.25	61.29	0.0	100.0	0.0	69.0		29.5 protein.degradation	chloroplast	Y	C	plastid stroma	
AT4G30920	926	AT4G30920.1	cytosol aminopeptidase family protein	583	STR		6.61	61.3	0.0	100.0	0.0	150.0		29.5 protein.degradation	chloroplast	Y	C	plastid	

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AT4G30950	927	AT4G30950.1	FAD6 (FATTY ACID DESATURASE 6); omega-6 fatty acid desaturase	448	ENV	Ch/E/IM	9.01	51.22	100.0	0.0	0.0	107.0	metabolism lipid	11.2.4 lipid metabolism.FA desaturation.omega 6 desaturase	chloroplast	Y	C	envelope-inner-integral	3.0
AT4G31780	928	AT4G31780.2	MGD1 (MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 1, MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE A); 1,2-diacylglycerol 3-beta-galactosyltransferase/ transferase, transferring glycosyl groups	504	ENV	Ch/E/IM	9.03	55.43	100.0	0.0	0.0	22.0	metabolism lipid	11.10.1 lipid metabolism.glycolipid synthesis.MGDG synthase	chloroplast	Y	C	envelope-inner	
AT4G31990	929	AT4G31990.1	ASP5 (ASPARTATE AMINOTRANSFERASE 5)	453	STR	Ch/S	8.18	49.83	1.1876828756345 5	98.812317124365 5	0.0	353.0	metabolism aa Asp	13.1.1.2.1 amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	undefined	Y	C	plastid stroma	

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AT4G32250	930	AT4G32250.1	protein kinase family protein	611	ENV	Ch/E ?	7.94	68.15	100.0	0.0	0.0	8.0	protein modification	29.4.1 protein.postranslational modification.kinase	undefined			-	1.0
AT4G32260	931	AT4G32260.1	ATP synthase family	219	THY-ENV	Ch/Th	5.79	23.91	25.245498737068 2	0.0	74.754501262931 8	165.0	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	chloroplast	Y	C	thylakoid-integral	1.0
AT4G32400	932	AT4G32400.1	SHS1 (SODIUM HYPERSENSITIVE 1); binding / transporter	392	ENV	Ch/E/IM	9.41	42.57	100.0	0.0	0.0	22.0	transporter MCF ATP/ADP ?	34.8 transport.metabolite transporters at the envelope membrane	undefined	Y		envelope-inner-integral	
AT4G32520	933	AT4G32520.1	SHM3 (SERINE HYDROXYMETHYLTRANSFERASE 3); glycine hydroxy methyltransferase	529	STR		9.03	57.98	0.0	100.0	0.0	10.0		1.2.5 PS.photorespiration.serine hydroxy methyltransferase	chloroplast	Y	C	-	
AT4G32590	934	AT4G32590.1	ferredoxin-related	173			9.25	18.66	0.0	100.0	0.0	1.0		1.1.5.2 PS.lightreaction.other electron carrier (ox/red).ferredoxin	chloroplast	Y	C	-	
AT4G32770	935	AT4G32770.1	VTE1 (VITAMIN E DEFICIENT 1)	488	ENV-THY	Ch/E & PG	5.94	54.72	70.799506096619 9	0.0	29.200493903380 1	10.0	metabolism vitamin and pigment	16.1.3.4 secondary metabolism.isoprenoids.tocopherol biosynthesis.tocopherol cyclase	chloroplast	Y	C	plastoglobules	

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AT4G33010	936	AT4G33010.1	ATGLDP1 (ARABIDOPSIS THALIANA GLYCINE DECARBOXYLASE P-PROTEIN 1); glycine dehydrogenase (decarboxylating)	1037	STR-THY		6.5	112.92	0.0	69.466080433718 1	30.533919566281 8	29.0		13.2.5.2 amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	undefined		M	mitochondria	
AT4G33030	937	AT4G33030.1	SQD1 (sulfoquinovosyldiacylglycerol 1); UDPsulfoquinovose synthase	477			8.41	53.11	0.0	100.0	0.0	6.0		11.10.3 lipid metabolism.glycolipid synthesis.UDP-sulfoquinovose synthase	chloroplast	Y	C	-	
AT4G33090	938	AT4G33090.1	APM1 (AMINOPEPTIDASE M1)	879			5.33	98.18	0.0	0.0	100.0	3.0		29.5 protein.degradation	undefined			-	
AT4G33350	939	AT4G33350.1	chloroplast inner membrane import protein Tic22, putative	268	ENV	Ch/E/IM	9.31	30.1	100.0	0.0	0.0	36.0	protein targeting Tic	29.3.3 protein.targeting.chloroplast	undefined	Y	C	envelope-intermembranespace	
AT4G33460	940	AT4G33460.1	ATNAP13 (EMBRYO DEFECTIVE 2751)	271	ENV	Ch/E/IM	8.68	29.62	100.0	0.0	0.0	8.0	transporter ABC	34.16 transport.ABC transporters and multidrug resistance systems	chloroplast	Y	C	-	

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AT4G33510	941	AT4G33510.1	DHS2 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE); 3-deoxy-7-phosphoheptulonate synthase	507	THY		8.93	56.15	0.0	3.9039802368323 3	96.096019763167 7	10.0		13.1.6.1.1 amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabino-heptulosonate 7-phosphate synthase	undefined	Y	C	-	
AT4G33520	942	AT4G33520.2	PAA1 (metal-transporting P-type ATPase 1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	949	ENV	Ch/E & Ch/S	8.97	99.99	100.0	0.0	0.0	43.0	transporter ATPase Cu	34.12 transport.metal	chloroplast	Y	C	envelope-inner	
AT4G33680	943	AT4G33680.1	AGD2 (ABERRANT GROWTH AND DEATH 2); transaminase	461	STR		7.02	50.39	0.0	100.0	0.0	123.0		13.1.3.5.3 amino acid metabolism.synthesis.aspartate family.lysine.LL-diaminopimelic acid aminotransferase	chloroplast	Y	C	plastid stroma	

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AT4G33760	944	AT4G33760.1	tRNA synthetase class II (D, K and N) family protein	664			6.73	74.51	0.0	100.0	0.0	7.0		29.1.12 protein.aa activation.aspartate-tRNA ligase	undefined	Y	C	mitochondria; plastid stroma	
AT4G34090	945	AT4G34090.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23370.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47838.1)	330	STR		5.65	36.91	0.0	100.0	0.0	38.0		35.2 not assigned. unknown	undefined		C	plastid stroma	
AT4G34120	946	AT4G34120.1	LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1)	238	STR		7.93	25.95	0.0	100.0	0.0	26.0		35.1 not assigned. no ontology	chloroplast	Y	C	plastid stroma	

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AT4G34200	947	AT4G34200.1	EDA9 (embryo sac development arrest 9); NAD binding / amino acid binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor / phosphoglycerate dehydrogenase	603	STR	Ch/S & other	6.16	63.32	3.5058190754393 3	96.494180924560 7	0.0	243.0	metabolism aa Ser	13.1.5.1.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	chloroplast	Y	C	plastid	
AT4G34240	948	AT4G34240.1	ALDH3I1 (Aldehyde dehydrogenase 3I1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	550	ENV	Ch/E & Ch/S	8.73	60.17	95.409112858803 3	0.0	4.5908871411966 5	21.0	metabolism carbon	5.10 fermentation.aldehyde dehydrogenase	undefined	Y		-	2.0
AT4G34290	949	AT4G34290.1	SWIB complex BAF60b domain-containing protein	144			9.79	15.99	0.0	24.528678553158 6	75.471321446841 4	4.0		35.1 not assigned. no ontology	chloroplast	Y	C	-	

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AT4G34350	950	AT4G34350.1	CLB6 (CHLOROPLAST BIOGENESIS 6); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase	466	STR		5.76	52.78	0.0	100.0	0.0	36.0		16.1.1.7 secondary metabolism.isoprenoids.non-mevalonate pathway.HDR	undefined	Y	C	plastid stroma	
AT4G34620	951	AT4G34620.1	SSR16 (ribosomal protein S16); structural constituent of ribosome	113	Mix	Ch/S	9.8	12.69	40.669085873078	45.0988310073189	14.232083119603 1	66.0	translation stroma	29.2.1.1.3.1.16 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S16	mitochondrion		M	mitochondria; plastid	
AT4G34740	952	AT4G34740.1	ATASE2 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 2); amidophosphoribosyltransferase	561	STR		6.29	61.03	0.0	100.0	0.0	45.0		23.1.2.1 nucleotide metabolism.synthesis.purine.amidophosphoribosyltransferase	chloroplast	Y	C	plastid	
AT4G34820	953	AT4G34820.1	-	1089	ENV	CH/E ?	9.22	35.72	100.0	0.0	0.0	2.0	unknown	-	undefined	Y		-	

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AT4G35000	954	AT4G35000.1	APX3 (ASCORBATE PEROXIDASE 3); L-ascorbate peroxidase	287	ENV	Ch/E ?	6.46	31.57	100.0	0.0	0.0	14.0	stress oxidative	21.2.1 redox.ascorbate and glutathione.ascorbate	undefined			peroxisome	1.0
AT4G35090	955	AT4G35090.1	CAT2 (CATALASE 2); catalase	492	STR	other	6.62	56.93	7.9235079517166 2	76.825986230232 9	15.250505818050 4	93.0	stress oxidative	21.6 redox.dismutases and catalases	undefined	Y		peroxisome	
AT4G35100	956	AT4G35100.1	PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	280	ENV	other	8.97	29.74	100.0	0.0	0.0	1.0	transporter aquaporin	34.19.1 transport.Major Intrinsic Proteins.PIP	other (e.g. cytoplasm)			plasma membrane	6.0
AT4G35250	957	AT4G35250.1	vestitone reductase-related	395	THY	Ch/E/IM	8.7	43.72	8.8832502557448 5	2.7784388901672 5	88.3383108540879	82.0	protein targeting ?	35.1 not assigned.no ontology	chloroplast	Y	C	thylakoid	
AT4G35630	958	AT4G35630.1	PSAT (phosphoserine aminotransferase); phosphoserine transaminase	430	STR		8.25	47.36	0.0	100.0	0.0	43.0		13.1.5.1.2 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoserine aminotransferase	chloroplast	Y	C	-	
AT4G36150	959	AT4G36150.1	disease resistance protein (TIR-NBS-LRR class), putative	1179			7.38	134.07	0.0	0.0	100.0	2.0		20.1.7 stress.biotic.PR-proteins	chloroplast	Y	C	-	1.0

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AT4G36530	960	AT4G36530.1	hydrolase, alpha/beta fold family protein	321	ENV	Ch/E	5.7	35.77	85.108250323708	0.0	14.891749676292	15.0	hydrolase ?	35.1 not assigned. no ontology	chloroplast			-	
AT4G36810	961	AT4G36810.1	GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltranstransferase	371			6.16	40.17	0.0	100.0	0.0	5.0		16.1.1.10 secondary metabolism.isoprenoids.mevalonate pathway. geranylgeranyl pyrophosphate synthase	chloroplast	Y	C	plastid stroma	
AT4G37000	962	AT4G37000.1	ACD2 (ACCELERATED CELL DEATH 2)	319	STR		5.71	36.44	0.0	100.0	0.0	17.0		19.50* tetrapyrrole degradation	chloroplast	Y	C	mitochondria; plastid stroma	
AT4G37200	963	AT4G37200.1	HCF164 (High chlorophyll fluorescence 164); thiol-disulfide exchange intermediate	261			5.26	28.74	0.0	0.0	100.0	5.0		29.8 protein assembly and cofactor ligation	undefined	Y	C	thylakoid-peripheral-stromal-side	
AT4G37270	964	AT4G37270.1	HMA1 (Heavy metal ATPase 1); copper-exporting ATPase	819	ENV	Ch/E/IM	8.05	88.19	100.0	0.0	0.0	12.0	transporter ATPase Cu	34.12 transport. metal	undefined	Y	M	envelope	6.0

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AT4G37930	965	AT4G37930.1	SHM1 (SERINE HYDROXYMETHYLTRANSFERASE 1); glycine hydroxymethyltransferase/poly(U) binding	517	THY-STR		8.12	57.4	0.0	32.773557540024 3	67.226442459975 7	22.0		25.1 C1-metabolism.glycine hydroxymethyltransferase	undefined		M	mitochondria	
AT4G38460	966	AT4G38460.1	GGR (GERANYLGERANYL REDUCTASE); farnesyltranstransferase	326			5.73	35.18	0.0	100.0	0.0	4.0		16.1.1.10 secondary metabolism.isoprenoids.mevalonate pathway.geranylgeranyl pyrophosphate synthase	chloroplast	Y	C	plastid stroma	
AT4G38510	967	AT4G38510.1	(VACUOLAR ATP SYNTHASE SUBUNIT B2); hydrogen ion transporting ATP synthase, rotational mechanism	487	ENV	Ch/E & other	5.03	54.3	100.0	0.0	0.0	37.0	transporter ATPase	34.1.1 transport.p- and v-ATPases.H+-transporting two-sector ATPase	other (e.g. cytoplasm)			-	
AT4G38950	968	AT4G38950.1	kinesin motor family protein	836			7.23	94.46	0.0	100.0	0.0	1.0		31.1 cell.organisation	undefined			-	
AT4G38970	969	AT4G38970.1	fructose-bisphosphate aldolase, putative	398	STR	Ch	6.78	42.98	15.219148713390 3	72.012305878043 1	12.768545408566 6	1114.0	metabolism carbon	1.3.6 PS.calvin cyle.aldolase	chloroplast	Y	C	plastid stroma; plastoglobules	

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AtCg00570	1295	AtCg00570	PSII cytochrome b559	39			10.73	4.42	0.0	0.0	100.0	6.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	secreted		C	thylakoid-integral	
AT4G39080	970	AT4G39080.1	VHA-A3 (VACUOLAR PROTON ATPASE A3); ATPase	821	ENV	other	5.65	92.83	100.0	0.0	0.0	16.0	transporter ATPase	34.1 transport.p- and v-ATPases	undefined			-	6.0
AT4G39120	971	AT4G39120.1	inositol monophosphatase family protein	346			6.02	38.23	0.0	100.0	0.0	9.0		3.4.5 minor CHO metabolism.myo-inositol.inositol phosphatase	chloroplast	Y	C	plastid	
AT4G39260	972	AT4G39260.1	ATGRP8/GR-RBP8 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 1, GLYCINE-RICH PROTEIN 8); RNA binding	169	THY		5.57	16.57	0.0	0.0	100.0	21.0		27.3.75 RNA.regulation of transcription.GRP	undefined			-	

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AT4G39460	973	AT4G39460.1	SAMC1/SAMT1 (S-ADENOSYLMETHIONINE CARRIER 1); S-adenosylmethionine transmembrane transporter/ binding	325	ENV	Ch/E & other	9.68	34.86	91.221248300535	0.0	8.7787516994649 9	24.0	transporter MCF SAM	34.8 transport.metabolite transporters at the envelope membrane	undefined	Y	C	envelope-inner-integral	5.0
AT4G39710	974	AT4G39710.1	immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative	217		Lum	8.44	23.26	0.0	0.0	100.0	6.0		29.6 protein.folding	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT4G39960	975	AT4G39960.1	DNAJ heat shock family protein	447	ENV	Ch/E & Ch/Th	9.22	48.03	89.262026088071 9	10.737973911928 1	0.0	18.0	chaperone and protease	26.29* misc.DnaJ domain with unknown function	undefined	Y	M	thylakoid	
AT4G39970	976	AT4G39970.1	haloacid dehalogenase-like hydrolase family protein	316	STR		5.39	34.65	0.0	100.0	0.0	13.0		3.2 minor CHO metabolism.trehalose	chloroplast	Y	C	plastid stroma	

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AT5G01220	977	AT5G01220.1	SQD2 (SULFOQUINOVOSYLDIACYLGLYCEROL 2); UDP-sulfoquinovose:DAG sulfoquinovosyltransferase/transferase, transferring glycosyl groups	510	ENV	Ch/E/IM	8.61	56.63	94.642361563425 7	0.0	5.3576384365743 3	36.0	metabolism lipid	11.10.4 lipid metabolism.glycolipid synthesis.sulfolipid synthase	chloroplast	Y	C	-	1.0
AT5G01500	978	AT5G01500.1	mitochondrial substrate carrier family protein	415	ENV	Ch/E/IM	9.81	45.09	94.924902288475	0.0	5.075097711525	19.0	transporter MCF ATP/ADP?	34.9 transport.metabolite transporters at the mitochondrial membrane	chloroplast	Y	C	-	3.0
AT5G01530	979	AT5G01530.1	chlorophyll A-B binding protein CP29 (LHCB4)	290	THY	Ch/Th	5.76	31.14	2.2570245713616 5	0.0	97.742975428638 3	762.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0
AT5G01590	980	AT5G01590.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO63840.1)	424	ENV	Ch/E/IM	6.38	48.87	100.0	0.0	0.0	64.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	
AT5G01600	981	AT5G01600.1	ATFER1 (FERRETIN 1); ferric iron binding	255	STR		5.73	28.17	0.0	100.0	0.0	16.0		15.2 metal handling.binding, chelation and storage	chloroplast	Y	C	plastid stroma	

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AT5G01920	982	AT5G01920.1	STN8 (state transition 8); kinase	495			9.42	54.97	0.0	0.0	100.0	3.0		1.1.30 PS.lightreaction.state transition	chloroplast	Y	C	thylakoid-integral	
AT5G02120	983	AT5G02120.1	OHP (ONE HELIX PROTEIN)	110			9.56	12.01	0.0	0.0	100.0	4.0		1.1.8* light stress chlorophyll binding	chloroplast	Y	C	thylakoid-integral	1.0
AT5G02240	984	AT5G02240.1	binding / catalytic/ coenzyme binding	253	STR		6.19	27.1	0.0	100.0	0.0	22.0		35.2 not assigned. unknown	undefined			-	
AT5G02490	985	AT5G02490.1	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)	653	ENV-STR	Ch/E & other	5.03	71.38	73.878747906397 8	26.121252093602 2	0.0	104.0	chaperone and protease	29.6 protein.folding	other (e.g. cytoplasm)			-	
AT5G02500	986	AT5G02500.1	HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding	651	ENV-STR	Ch/E & other	5.02	71.35	72.065627646203 8	26.833531905551 7	1.100840448244 5 8	147.0	chaperone and protease	29.6 protein.folding	other (e.g. cytoplasm)			cytosol	

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AT5G02940	987	AT5G02940.1	similar to phosphotransferase-related [Arabidopsis thaliana] (TAIR:AT5G43745.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71282.1); similar to hypothetical protein OsI_009890 [Oryza sativa (indica cultivar-group)] (GB:EAY88657.1); s	813	ENV	Ch/E ?	7.53	92.13	98.490711080186 2	0.0	1.5092889198137 5	319.0	transporter ion channel ?	35.2 not assigned. unknown	undefined	Y	M	envelope	3.0
AT5G03300	988	AT5G03300.1	ADK2 (ADENOSINE KINASE 2); kinase	345			5.14	37.84	0.0	100.0	0.0	7.0		23.3.2.1 nucleotide metabolism.salvage.nucleoside kinases.adenosine kinase	undefined			-	
AT5G03630	989	AT5G03630.1	ATMDAR2; monodehydroascorbate reductase (NADH)	435	STR		5.24	47.48	0.0	100.0	0.0	14.0		21.2.1 redox.ascorbate and glutathione.ascorbate	undefined			-	

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AT5G03650	990	AT5G03650.1	SBE2.2 (STARCH BRANCHING ENZYME 2.2); 1,4-alpha-glucan branching enzyme	716			5.45	82.83	0.0	100.0	0.0	4.0		2.1.2.3 major CHO metabolism.synthesis.starch.starch branching	undefined			plastid stroma	
AT5G03880	991	AT5G03880.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10000.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15903.1); contains InterPro domain Thioredoxin-like	339	ENV-THY	Ch/E & Ch/Th	9.01	37.04	58.827097858819 8	0.0	41.172902141180 3	26.0	redox ?	21.4 redox.glutaredoxins	chloroplast	Y	C	thylakoid	2.0

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AT5G03900	992	AT5G03900.2	Identical to Uncharacterized protein At5g03900 precursor [Arabidopsis Thaliana] (GB:Q8GW20;GB:Q8L632;GB:Q8LG15;GB:Q9FFM9;GB:Q9LZB9); similar to unnamed protein product [Vitis vinifera] (GB:CAO15906.1); contains InterPro domain HesB/YadR/YfhF-like (In	429	ENV	Ch/E/IM	8.88	48.17	88.690765632081 2	2.7740057449301 4	8.5352286229886 8	12.0	unknown	35.2 not assigned. unknown	undefined	Y	C	-	3.0
AT5G03910	993	AT5G03910.1	ATATH12 (Arabidopsis ABC transporter homolog 12); ATPase, coupled to transmembrane movement of substances	634	ENV	Ch/E/IM	9.05	69.19	100.0	0.0	0.0	63.0	transporter ABC	34.16 transport. ABC transporters and multidrug resistance systems	chloroplast	Y	C	-	6.0

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AT5G03940	994	AT5G03940.1	FFC (FIFTY-FOUR CHLOROPLAST HOMOLOGUE); 7S RNA binding / GTP binding / mRNA binding	564	STR		9.47	61.23	0.0	95.701319601358 7	4.2986803986413 5	144.0		29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	plastid stroma	
AT5G04140	995	AT5G04140.1	GLS1/GLU1/GLUS (FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1); glutamate synthase (ferredoxin)	1622	STR	Ch/S	5.93	176.75	3.9749742873428 4	94.932068818435 9	1.0929568942213 2	1626.0	metabolism carbon	12.2.1.1 N-metabolism.ammonia metabolism.glutamate synthase.ferredoxin dependent	chloroplast	Y	C	plastid stroma	
AT5G04360	996	AT5G04360.1	ATLDA/ATPU1 (PULLULANASE 1); alpha-amylase/limit dextrinase	965	STR		5.93	107.06	0.0	100.0	0.0	10.0		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	chloroplast	Y	C	plastid	
AT5G04590	997	AT5G04590.1	SIR (sulfite reductase); sulfite reductase (ferredoxin)	642	STR	Ch/S	8.5	71.95	6.1252492357109 1	93.874750764289 1	0.0	179.0	metabolism aa Cys	14.3 S-assimilation.sulfite redox	chloroplast	Y	C	plastid stroma	
AT5G04710	998	AT5G04710.1	aspartyl aminopeptidase, putative	526	STR		6.49	57.86	0.0	100.0	0.0	21.0		29.5.4 protein.degradation.aspartate protease	chloroplast	Y	C	-	

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AT5G04740	999	AT5G04740.1	ACT domain-containing protein	301	STR		5.26	33.24	0.0	100.0	0.0	29.0		13 amino acid metabolism	chloroplast	Y	C	plastid stroma	
AT5G04830	1000	AT5G04830.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96633.1); contains domain SSF54427 (SSF54427)	178	ENV	CH/E ?	8.43	20.29	100.0	0.0	0.0	4.0	unknown	35.2 not assigned. unknown	other (e.g. cytoplasm)			-	
AT5G04900	1001	AT5G04900.1	short-chain dehydrogenase/reductase (SDR) family protein	348	ENV	Ch/E & Ch/S	9.49	38.14	100.0	0.0	0.0	4.0	redox ?	19.50* tetrapyrrole degradation	chloroplast	Y	C	thylakoid	
AT5G05000	1002	AT5G05000.1	ATTOC34/OEP34 (Translocase of chloroplast 34)	313	ENV	Ch/E/OM	9.42	34.7	98.562837042782 2	0.0	1.4371629572178 3	67.0	protein targeting Toc	29.3.3 protein.targeting.chloroplast	undefined			envelope-outer-integral	
AT5G05570	1003	AT5G05570.1	transducin family protein / WD-40 repeat family protein	1124			5.47	122.66				2.0		35.1 not assigned. no ontology	undefined		M	-	
AT5G05730	1004	AT5G05730.1	ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1); anthranilate synthase	595	STR		6.08	66.31	0.0	100.0	0.0	26.0		13.1.6.5.1 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate synthase	undefined	Y	C	-	

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AT5G05740	1005	AT5G05740.1	ATEGY2; metalloendopeptidase	556			4.98	60.06	0.0	0.0	100.0	4.0		29.5.7 protein.degradation.metalloprotease	undefined	Y	C	thylakoid	6.0
AT5G06130	1006	AT5G06130.1	chaperone protein dnaJ-related	231			8.68	25.44	0.0	0.0	100.0	1.0		26.29* misc.DnaJ domain with unknown function	chloroplast			-	2.0
AT5G06220	1007	AT5G06220.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11560.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11560.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11560.4); similar to Os08g0482100 [Oryza sativa (j	813	ENV	Ch/E ?	5.47	90.31	100.0	0.0	0.0	18.0	transporter K+/H+?	35.2 not assigned. unknown	undefined			-	3.0
AT5G06290	1008	AT5G06290.1	2-cys peroxiredoxin, chloroplast, putative	273	STR	Ch/S	5.54	29.78	13.309294843392 3	85.526313417722 7	1.1643917388849 8	356.0	redox	21.5 redox.peiredoxins	chloroplast	Y	C	plastid stroma	
AT5G06430	1009	AT5G06430.1	thioredoxin-related	194	ENV	Ch/E & Ch/S	9.4	21.75	100.0	0.0	0.0	2.0	redox ?	21.1 redox.thioredoxin	undefined	Y	C	-	

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AT5G06670	1010	AT5G06670.1	kinesin motor protein-related	992			5.74	110.71	0.0	100.0	0.0	1.0		31.1 cell.organisation	chloroplast	Y	C	-	
AT5G07020	1011	AT5G07020.1	proline-rich family protein	235			4.71	24.39	0.0	0.0	100.0	7.0		35.1.42 not assigned. no ontology. proline rich family	undefined	Y		thylakoid	1.0
AT5G07760	1012	AT5G07760.1	formin homology 2 domain-containing protein / FH2 domain-containing protein	853	STR		7.42	95.54	0.0	100.0	0.0	10.0		35.1.20 not assigned. no ontology. formin homology 2 domain-containing protein	chloroplast	Y	C	-	
AT5G08050	1013	AT5G08050.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO62462.1); similar to unknown [Populus trichocarpa] (GB:ABK95457.1); contains InterPro domain Protein of unknown function DUF1118 (InterPro:IPR009500); contains InterPro domain Uncharacterised	158	THY		9.3	16.58	0.0	0.0	100.0	32.0		35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	2.0

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AT5G08280	1014	AT5G08280.1	HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane synthase	382	STR	Ch/E & Ch/S	8.75	41.04	4.4697118791563 9	95.530288120843 6	0.0	312.0	metabolism vitamin and pigment	19.5 tetrapyrrole synthesis.porphobilinogen deaminase	chloroplast	Y	C	plastid stroma	
AT5G08540	1015	AT5G08540.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO65975.1)	346	ENV	Ch/E & Ch/Th	5.67	38.65	97.286254338170 4	0.0	2.7137456618296 2	75.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	envelope	1.0
AT5G08650	1016	AT5G08650.1	GTP-binding protein LepA, putative	681			6.29	75.43	0.0	66.102150838928 1	33.897849161071 9	7.0		29.2.4 protein.synthesis.elongation	chloroplast	Y	C	plastid stroma	
AT5G08680	1017	AT5G08680.1	ATP synthase beta chain, mitochondrial, putative	559	THY-ENV	other	6.06	59.86	23.408071848239 5	14.642815477345 7	61.949112674414 8	50.0	transporter ATPase	9.9 mitochondrial electron transport / ATP synthesis.F1-ATPase	undefined	Y	M	mitochondria	
AT5G08740	1018	AT5G08740.1	NDC1 (NAD(P)H DEHYDROGENASE C1); NADH dehydrogenase	519	THY	Ch/E & other	6.51	56.85	13.782973726184 4	0.0	86.217026273815 6	15.0	metabolism nucleotide ?	35 not assigned; 9.2.3 mitochondrial electron transport / ATP synthesis.NADH-DH.type II.mitochondrial	chloroplast	Y	C	plastoglobules; mitochondria	

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AT5G09650	1019	AT5G09650.1	ATPPA6 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 6); inorganic diphosphatase/ pyrophosphatase	300	STR	Ch/S	5.71	33.38	4.9418038221202 3	95.058196177879 8	0.0	149.0	metabolism Pi	23.4.99 nucleotide metabolism.phosphotransfer and pyrophosphatases .misc	undefined	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT5G09660	1020	AT5G09660.1	PMDH2 (PEROXISOMAL NAD-MALATE DEHYDROGENASE 2); malate dehydrogenase	354	ENV-THY	other	8.14	37.37	57.734035671315	2.5796621310144 4	39.686302197670 6	28.0	metabolism carbon	6.3 gluconeogenesis. Malate DH	undefined			peroxisome	
AT5G09810	1021	AT5G09810.1	ACT7 (actin 7)	377	STR-ENV	Ch/E & other	5.3	41.73	46.021489832368 7	53.978510167631 3	0.0	20.0	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT5G09995	1022	AT5G09995.2	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G08530.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81396.1)	205	ENV	Ch/E/IM	9.5	22.44	100.0	0.0	0.0	3.0	unknown	35.2 not assigned. unknown	undefined	Y	C	-	1.0

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AT5G10160	1023	AT5G10160.1	beta-hydroxyacyl-ACP dehydratase, putative	219	THY-ENV	Ch/E ?	9.32	24.12	34.191349113866 8	0.0	65.808650886133 2	14.0	metabolism lipid	11.1.5 lipid metabolism.FA synthesis and FA elongation.beta hydroxyacyl ACP dehydratase	chloroplast	Y	C	-	
AT5G10450	1024	AT5G10450.1	GRF6 (G-BOX REGULATING FACTOR 6); protein phosphorylated amino acid binding	248			4.76	27.97	0.0	100.0	0.0	7.0		30.7 signalling.14-3-3 proteins	undefined			-	
AT5G10490	1025	AT5G10490.1	MSL2 (MSCS-LIKE 2)	673	ENV	Ch/E/IM	9.57	74.42	100.0	0.0	0.0	1.0	transporter ion channel	31.2.5 cell.division.plastid	chloroplast	Y	C	envelope	2.0
AT5G10920	1026	AT5G10920.1	argininosuccinate lyase, putative / arginosuccinase, putative	517	STR		5.59	57.51	0.0	100.0	0.0	12.0		13.1.2.3.23 amino acid metabolism.synthesis.glutamate family.arginine.argininosuccinate lyase	chloroplast	Y	C	-	
AT5G11520	1027	AT5G11520.1	ASP3 (ASPARTATE AMINOTRANSFERASE 3)	449			9.34	48.95	0.0	49.367597204202 1	50.632402795797 9	9.0		13.1.1.2.1 amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	undefined	Y	C	peroxisome	

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AT5G11880	1028	AT5G11880.1	diaminopimelate decarboxylase, putative / DAP carboxylase, putative	489	STR		6.21	54.16	0.0	100.0	0.0	64.0		13.1.3.5.5 amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate decarboxylase	chloroplast	Y	C	plastid	
AT5G12040	1029	AT5G12040.1	carbon-nitrogen hydrolase family protein	369	STR		8.78	40.33	0.0	100.0	0.0	30.0		35.1 not assigned. no ontology	chloroplast	Y	C	plastid stroma	
AT5G12470	1030	AT5G12470.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40400.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40400.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21888.1)	386	ENV	Ch/E/IM	7.01	41.32	93.849397757344 7	0.0	6.1506022426553 5	303.0	unknown	34.8 transport. metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope	4.0

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AT5G12860	1031	AT5G12860.1	DIT1 (DICARBOXYLATE TRANSPORTER 1); oxoglutarate:malate antiporter	557	ENV-THY	Ch/E/IM	9.75	59.21	81.755752105715 2	0.0	18.244247894284 8	174.0	transporter oxoglut/mal	34.8 transport. metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	14.0
AT5G13030	1032	AT5G13030.1	similar to hypothetical protein OsI_021963 [Oryza sativa (indica cultivar-group)] (GB:EAZ00731.1); similar to Os06g0320700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057514.1); similar to predicted protein [Physcomitrella patens subsp. patens	633	STR		6.27	71.09	0.0	100.0	0.0	25.0		35.2 not assigned. unknown	undefined	Y	C	plastid stroma	

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AT5G13110	1033	AT5G13110.1	G6PD2 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 2); glucose-6-phosphate dehydrogenase	596	STR		8.45	67.16	0.0	100.0	0.0	19.0		7.1.1 OPP.oxidative PP.G6PD	chloroplast	Y	C	-	
AT5G13120	1034	AT5G13120.1	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	259	THY	Lum	9.38	28.3	0.0	9.7746155337778 4	90.225384466222 2	19.0		29.6 protein.folding	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT5G13280	1035	AT5G13280.1	AK-LYS1 (ASPARTATE KINASE 1)	569	STR		6.37	62.29	0.0	100.0	0.0	17.0		13.1.3.6.1.1 amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate kinase	chloroplast	Y	C	-	
AT5G13410	1036	AT5G13410.1	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	256		Lum	7.54	27.77				2.0		29.6 protein.folding	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT5G13420	1037	AT5G13420.1	transaldolase, putative	438	STR		6.07	47.69	0.0	100.0	0.0	27.0		7.2.2 OPP.non-reductive PP.transaldolase	chloroplast	Y	C	-	1.0

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AT5G13490	1038	AT5G13490.1	AAC2 (ADP/ATP CARRIER 2); ATP:ADP antiporter / binding	385			9.79	41.74	0.0	0.0	100.0	6.0		34.14 transport.unspecified cations	undefined			-	3.0
AT5G13510	1039	AT5G13510.1	ribosomal protein L10 family protein	220	STR-ENV	Ch/S	9.36	24.73	26.581489498522 1	63.186144667558 8	10.232365833919 1	131.0	translation stroma	29.2.1.1.1.2.10 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L10	chloroplast	Y	C	plastid ribosome	
AT5G13630	1040	AT5G13630.1	GUN5 (GENOMES UNCOUPLED 5)	1381	Mix	Ch/E & other	5.79	153.57	44.902890573317 9	47.240261193796 9	7.856848232885 2 5	61.0	metabolism vitamin and pigment & hormone	19.10 tetrapyrrole synthesis.magnesium chelatase	chloroplast	Y	C	plastid	
AT5G13650	1041	AT5G13650.1	elongation factor family protein	675	STR		6.85	74.31	0.0	100.0	0.0	48.0		29.2.4 protein.synthesis.elongation	chloroplast	Y	C	plastid stroma	
AT5G13720	1042	AT5G13720.1	structural constituent of ribosome	262	ENV	Ch/E/IM	9.02	28.91	99.561407067515 1	0.438592932484879	0.0	72.0	unknown	29.2.1.99.99 protein.synthesis.ribosomal protein.unknown.unknown	chloroplast	Y	C	-	3.0
AT5G14060	1043	AT5G14060.1	CARAB-AK-LYS (Lysine-sensitive aspartate kinase); amino acid binding / aspartate kinase	544	STR		6.31	59.6	0.0	100.0	0.0	13.0		13.1.3.6.1.1 amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate kinase	undefined	Y	C	-	

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AT5G14100	1044	AT5G14100.1	ATNAP14 (Non-intrinsic ABC protein 14)	278	ENV	Ch/E/IM	8.99	30.71	100.0	0.0	0.0	10.0	transporter ABC Co ?	34.16 transport.ABC transporters and multidrug resistance systems	chloroplast	Y	C	-	
AT5G14200	1045	AT5G14200.1	3-isopropylmalate dehydrogenase, chloroplast, putative	409	STR		5.74	44.16	0.0	100.0	0.0	81.0		13.1.4.4.3 amino acid metabolism.synthesis.branched chain group.leucine specific.3-isopropylmalate dehydrogenase	undefined			plastid stroma	
AT5G14220	1046	AT5G14220.1	HEMG2/MEE61 (maternal effect embryo arrest 61); oxidoreductase/ protoporphyrinogen oxidase	508	ENV	Ch/E ?	8.35	55.63	100.0	0.0	0.0	54.0	metabolism vitamin and pigment	19.9 tetrapyrrole synthesis.protoporphyrin IX oxidase	undefined			-	
AT5G14260	1047	AT5G14260.1	SET domain-containing protein	514	STR		6.38	57.58	0.0	100.0	0.0	35.0		27.3.69 RNA.regulation of transcription.SET-domain transcriptional regulator family	chloroplast	Y	C	plastid	

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AT5G14320	1048	AT5G14320.1	30S ribosomal protein S13, chloroplast (CS13)	169	STR	Ch/S	10.26	19.09	15.263174827671 7	84.736825172328 3	0.0	93.0	translation stroma	29.2.1.1.1.1.13 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S13	chloroplast	Y	C	plastid ribosome	
AT5G14590	1049	AT5G14590.1	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	485	STR-THY		8.05	54.19	0.0	79.592167235725 2	20.407832764274 8	13.0		8.1.4 TCA / org.transformation.TCA.IDH	undefined	Y	C	-	
AT5G14660	1050	AT5G14660.1	PDF1B (PEPTIDE DEFORMYLASE 1B); peptide deformylase	273			8.92	30.61	0.0	100.0	0.0	6.0		29.4 protein.postranslational modification	chloroplast	Y	C	mitochondria; plastid stroma	
AT5G14740	1051	AT5G14740.2	CA2 (BETA CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding	331	ENV-STR	Ch & other	7.06	36.61	59.222533146026 6	40.483687004291 5	0.293779849681838	830.0	metabolism carbon	8.3 TCA / org.transformation.carbonic anhydrases	undefined	Y		plastid stroma	

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AT5G14780	1052	AT5G14780.1	FDH (FORMATE DEHYDROGENASE); NAD binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	384			7.11	42.41	0.0	100.0	0.0	3.0		25.10 C1-metabolism.formate dehydrogenase	undefined	Y	M	mitochondria	
AT5G14910	1053	AT5G14910.1	heavy-metal-associated domain-containing protein	178	STR-ENV	Ch/S & Ch/Th	5.16	18.95	24.226403607846 9	75.773596392153 1	0.0	30.0	unknown	15.2 metal handling. binding, chelation and storage	chloroplast	Y	C	plastid stroma	
AT5G15450	1054	AT5G15450.1	APG6/CLPB-P/CLPB3 (ALBINO AND PALE GREEN 6); ATP binding / ATPase	968	STR		5.92	108.94	0.0	100.0	0.0	45.0		29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT5G15530	1055	AT5G15530.1	BCCP2 (biotin carboxyl carrier protein 2); biotin binding	255	STR-ENV	Ch/E/IM	7.64	27.28	43.221829853702 6	56.778170146297 4	0.0	28.0	metabolism lipid	11.1.1 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	chloroplast	Y	C	envelope-inner-peripheral-stromal-side	

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AT5G15880	1056	AT5G15880.1	similar to hypothetical protein [Cleome spinosa] (GB:ABD96950.1); contains InterPro domain Polyadenylate-binding protein/Hyperplastic disc protein; (InterPro:IPR002004)	348			5.32	39.57	0.0	100.0	0.0	2.0		35.2 not assigned. unknown	other (e.g. cytoplasm)			-	1.0
AT5G16010	1057	AT5G16010.1	3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein	268	ENV	Ch/E ?	9.37	30.12	96.558379660622 3	0.0	3.4416203393777 1	28.0	metabolism hormone brassinosteroid	17.3.1.1.1 hormone metabolism.brassinosteroid.synthesis-degradation.BRs.DET2	undefined			-	6.0
AT5G16150	1058	AT5G16150.1	GLT1/PGLCT (GLUCOSE TRANSPORTER 1); carbohydrate transmembrane transporter/ sugar:hydrogen ion symporter	546	ENV	Ch/E/IM	9.06	56.97	100.0	0.0	0.0	14.0	transporter glucose ?	34.8 transport. metabolite transporters at the envelope membrane	undefined	Y	C	envelope-inner-integral	12.0

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AT5G16390	1059	AT5G16390.1	BCCP/BCCP-1/BCCP1/CAC1-A/CAC1A (BIOTIN CARBOXYL CARRIER, BIOTIN CARBOXYL CARRIER PROTEIN 1); biotin binding	280	STR-ENV	Ch/E/IM	9.11	29.61	31.353766567662 4	68.646233432337 6	0.0	64.0	metabolism lipid	11.1.1 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	chloroplast	Y	C	envelope-inner-peripheral-stromal-side; plastid stroma	
AT5G16440	1060	AT5G16440.1	IPP1 (ISOPENTENYL DIPHOSPHATE ISOMERASE 1); isopentenyl-diphosphate delta-isomerase	291			5.68	33.21	0.0	100.0	0.0	2.0		16.1.2.7 secondary metabolism.isoprenoids.mevalonate pathway.isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	chloroplast	Y	C	cytosol; plastid	
AT5G16620	1061	AT5G16620.1	PDE120 (PIGMENT DEFECTIVE EMBRYO)	447	ENV	Ch/E & Ch/Th	5.37	48.9	94.462530467570 6	0.0	5.5374695324293 5	215.0	protein targeting Tic	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope-inner-integral	1.0

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AT5G16660	1062	AT5G16660.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02900.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62132.1)	168	ENV	Ch/E & Ch/Th	8.51	18.17	87.274363617285 2	0.0	12.725636382714 8	44.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	envelope	1.0
AT5G16710	1063	AT5G16710.1	DHAR3 (DEHYDROASCORBATE REDUCTASE 1); glutathione dehydrogenase (ascorbate)	258	STR	Ch/S	7.59	28.51	4.6204307859651 6	95.379569214034 8	0.0	79.0	redox	21.2.1 redox.ascorbate and glutathione.ascorbate	chloroplast	Y	C	plastid stroma	
AT5G16715	1064	AT5G16715.1	EMB2247 (EMBRYO DEFECTIVE 2247); ATP binding / aminoacyl-tRNA ligase	970	STR		5.95	110.27	0.0	100.0	0.0	35.0		29.1.9 protein.aa activation.valine-tRNA ligase	chloroplast	Y	C	plastid stroma	
AT5G17170	1065	AT5G17170.1	ENH1 (ENHANCER OF SOS3-1); metal ion binding	271	THY		9.59	28.45	0.0	0.0	100.0	25.0		29.8 protein assembly and cofactor ligation	chloroplast	Y	C	thylakoid	1.0

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AT5G17520	1066	AT5G17520.1	RCP1 (ROOT CAP 1)	415	ENV	Ch/E/IM	9.37	45.28	100.0	0.0	0.0	7.0	transporter maltose	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	9.0
AT5G17530	1067	AT5G17530.1	phosphoglucosamine mutase family protein	581	STR		5.86	62.87	0.0	100.0	0.0	22.0		4.2 glycolysis.PGM	undefined	Y	M	plastid stroma	
AT5G17560	1068	AT5G17560.1	BolA-like family protein	177			9.63	19.53	0.0	100.0	0.0	2.0		27.3 RNA.regulation of transcription	chloroplast	Y	C	plastid stroma	
AT5G17630	1069	AT5G17630.1	glucose-6-phosphate/phosphate translocator, putative	417	ENV	Ch/E/IM	9.71	45.77	100.0	0.0	0.0	19.0	transporter Pi/G6P	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	-	8.0
AT5G17670	1070	AT5G17670.1	hydrolase, acting on ester bonds	309	ENV-THY	Ch/E & other	5.57	33.4	50.959095857742 8	0.0	49.040904142257 2	4.0	metabolism lipid / vesicular trafficking ?	35.2 not assigned.unknown	undefined	Y	M	-	
AT5G17710	1071	AT5G17710.1	EMB1241 (EMBRYO DEFECTIVE 1241); adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization	324	STR		4.56	35.49	0.0	100.0	0.0	67.0		29.6 protein.folding	chloroplast	Y	C	plastid stroma	

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AT5G17920	1072	AT5G17920.1	ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/methionine synthase	765	STR		6.08	84.35	0.0	100.0	0.0	68.0		13.1.3.4 amino acid metabolism.synthesis.aspartate family.methionine	undefined			not plastid	
AT5G17990	1073	AT5G17990.1	TRP1 (TRYPTOPHAN BIOSYNTHESIS 1); anthranilate phosphoribosyltransferase	444	STR		6.9	46.52	0.0	100.0	0.0	40.0		13.1.6.5.2 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate phosphoribosyltransferase	chloroplast	Y	C	plastid stroma	
AT5G18660	1074	AT5G18660.1	DVR (PALE-GREEN AND CHLOROPHYLL B REDUCED 2); 3,8-divinyl protochlorophyllide a 8-vinyl reductase	417	ENV-THY	Ch/E/IM	7.47	45.89	74.516635175914 9	4.9943089806235 5	20.4890558434615	22.0	metabolism vitamin and pigment	19.13 tetrapyrrole synthesis.divinyl chlorophyllide-a 8-vinyl-reductase	chloroplast	Y	C	plastid	

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AT5G19220	1075	AT5G19220.1	ADG2 (ADPG PYROPHOSPHORYLASE 2); glucose-1-phosphate adenylyltransferase	522	STR		8.02	57.67	0.0	100.0	0.0	125.0		2.1.2.1 major CHO metabolism.synthesis.starch.AGPase	chloroplast	Y	C	plastid stroma	
AT5G19370	1076	AT5G19370.1	rhodanese-like domain-containing protein / PPIC-type PPIASE domain-containing protein	299			8.62	32.98	0.0	100.0	0.0	8.0		26.23 misc.rhodanese	undefined	Y	C	plastid	
AT5G19460	1077	AT5G19460.1	ATNUDT20 (Arabidopsis thaliana Nudix hydrolase homolog 20); hydrolase	374			7.56	41.92	0.0	100.0	0.0	2.0		26.13 misc.acid and other phosphatases	chloroplast	Y	C	plastid	
AT5G19620	1078	AT5G19620.1	OEP80 (ARABIDOPSIS THALIANA OUTER ENVELOPE PROTEIN OF 80 KDA)	732	ENV	Ch/E/OM	8.41	79.93	100.0	0.0	0.0	85.0	protein targeting Toc	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	envelope-outer	
AT5G19750	1079	AT5G19750.1	peroxisomal membrane 22 kDa family protein	288	ENV	Ch/E/IM	10.23	30.36	100.0	0.0	0.0	14.0	transporter ?	35.1 not assigned.no ontology	chloroplast	Y	C	-	3.0

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AT5G19850	1080	AT5G19850.1	hydrolase, alpha/beta fold family protein	359	ENV	Ch/E/IM	6.09	40.1	100.0	0.0	0.0	2.0	hydrolase ?	35.1 not assigned. no ontology	undefined	Y	C	-	
AT5G19855	1081	AT5G19855.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO21907.1)	203			9.67	23.47	0.0	100.0	0.0	5.0		35.2 not assigned. unknown	chloroplast	Y	C	-	
AT5G19940	1082	AT5G19940.1	plastid-lipid associated protein PAP-related / fibrillin-related	239	ENV-THY	Ch	9.49	26.48	70.613744275968 9	0.0	29.386255724031 1	61.0	PAP_fibrillin	26.31* misc.fibrillins	chloroplast	Y	C	plastid	
AT5G20130	1083	AT5G20130.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO21131.1)	202	ENV	Ch/E/IM	9.58	21.94	100.0	0.0	0.0	3.0	RNA binding ?	35.2 not assigned. unknown	undefined	Y	C	-	1.0
AT5G20140	1084	AT5G20140.1	SOUL heme-binding family protein	378	ENV-THY	Ch	6.98	43.16	62.442479562626 3	0.0	37.557520437373 7	16.0	unknown	21.3 redox.heme	chloroplast	Y	C	thylakoid	
AT5G20250	1085	AT5G20250.1	DIN10 (DARK INDUCIBLE 10); hydrolase, hydrolyzing O-glycosyl compounds	749			6.21	83.11	0.0	100.0	0.0	8.0		3.1.2.2 minor CHO metabolism.raffinose family.raffinose synthases.putative	undefined			-	

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AT5G20630	1086	AT5G20630.1	GLP3 (GERMIN-LIKE PROTEIN 3); manganese ion binding / metal ion binding / nutrient reservoir	211			6.25	21.83	0.0	0.0	100.0	2.0		20.2.99 stress.abiotic.unspecified	secreted		S	-	2.0
AT5G20720	1087	AT5G20720.1	CPN20 (CHAPERONIN 20); calmodulin binding	253	STR-ENV	Ch & other	8.85	26.8	41.47459764928	58.52540235072	0.0	274.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT5G21430	1088	AT5G21430.1	DNAJ heat shock N-terminal domain-containing protein	218	ENV-THY	Ch/E & Ch/Th	5.07	24.43	50.959095857742 8	0.0	49.040904142257 2	2.0	chaperone and protease	26.29* misc.DnaJ domain with unknown function	chloroplast	Y	C	thylakoid-integral	1.0
AT5G22210	1089	AT5G22210.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO48680.1)	80	ENV	CH/E ?	6.82	9.31	100.0	0.0	0.0	2.0	unknown	35.2 not assigned. unknown	undefined			-	
AT5G22510	1090	AT5G22510.1	beta-fructofuranosidase, putative / invertase, putative / sacchARase, putative / beta-fructosidase, putative	617			5.85	69.24	0.0	100.0	0.0	4.0		2.2.1.3.1 major CHO metabolism.degradation.sucrose.invertases.neutral	chloroplast	Y	C	plastid stroma	

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AT5G22620	1091	AT5G22620.1	phosphoglycerate/bisphosphoglycerate mutase family protein	482			6.64	53.11	0.0	100.0	0.0	5.0		4.11 lycolysis. phosphoglycerate mutase	chloroplast	Y	C	plastid stroma	
AT5G22640	1092	AT5G22640.1	EMB1211 (EMBRYO DEFECTIVE 1211)	871	ENV	Ch/E ?	4.36	99.95	100.0	0.0	0.0	51.0	RNA binding ?	35.1 not assigned. no ontology	other (e.g. cytoplasm)			-	
AT5G22790	1093	AT5G22790.1	RER1 (RETICULATA-RELATED 1)	433	ENV	Ch/E/IM	5.14	46.83	100.0	0.0	0.0	14.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	3.0
AT5G22800	1094	AT5G22800.1	EMB1030 (EMBRYO DEFECTIVE 1030); ATP binding / alanine-tRNA ligase/ ligase, forming aminoacyl-tRNA and related compounds / nucleic acid binding	978	STR		5.42	107.83	0.0	100.0	0.0	117.0		29.1.7 protein.aa activation .alanine-tRNA ligase	undefined	Y	C	mitochondria; plastid stroma	
AT5G22830	1095	AT5G22830.1	GMN10 (Arabidopsis thaliana Mg transporter 10)	459	ENV	Ch/E/IM	5.23	51.09	92.57574746789	0.0	7.4242525321100 2	39.0	transporter Mg	34.8 transport. metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	2.0

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AT5G23040	1096	AT5G23040.1	CDF1 (CELL GROWTH DEFECT FACTOR 1); heat shock protein binding	258	ENV	Ch/E & other	9.68	28.81	100.0	0.0	0.0	38.0	signalling ?	35.2 not assigned. unknown	chloroplast	Y	C	envelope	3.0
AT5G23060	1097	AT5G23060.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G59780.1); similar to extracellular Ca2+ sensing receptor [Glycine max] (GB:ABY57763.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)	387	THY		9.41	41.28	0.0	0.0	100.0	153.0		1.1.30 PS.lightreaction.state transition	chloroplast	Y	C	thylakoid-integral	1.0
AT5G23120	1098	AT5G23120.1	HCF136 (High chlorophyll fluorescence 136)	403	THY-ENV	Ch/Th/Lum	6.79	44.1	16.836989268282 4	0.526615196347433	82.636395535370 1	124.0	PS PSII	29.8 protein assembly and cofactor ligation	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	

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AT5G23890	1099	AT5G23890.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G52410.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO49433.1)	946	ENV	Ch/E & Ch/Th	4.61	103.92	100.0	0.0	0.0	97.0	unknown	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope	1.0
AT5G24020	1100	AT5G24020.1	MIND (ACCUMULATION AND REPLICATION OF CHLOROPLAST 11)	326	ENV-STR	CH/E/IM	7.58	35.69	76.174644552747 2	23.825355447252 8	0.0	10.0	plastid division	31.2.5 cell.division.plastid	chloroplast	Y	C	envelope-inner; plastid stroma	
AT5G24300	1101	AT5G24300.1	ATSS1/SSI (STARCH SYNTHASE I); transferase, transferring glycosyl groups	652	STR	Ch/S	6.01	72.09	7.4014252711539 2	92.598574728846 1	0.0	51.0	metabolism carbon	2.1.2.2 major CHO metabolism.synthesis.starch.starch synthase	chloroplast	Y	C	plastid stroma	
AT5G24400	1102	AT5G24400.1	EMB2024 (EMBRYO DEFECTIVE 2024); catalytic	325	STR		7.64	35.64	0.0	100.0	0.0	15.0		7.1.2 OPP.oxidative PP.6-phosphogluconolactonase	chloroplast	Y	C	plastid stroma	

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AT5G24490	1103	AT5G24490.1	30S ribosomal protein, putative	308	THY-STR	Ch/S	6.29	34.85	9.4665751369525	22.206652767822 3	68.326772095225 2	37.0	translation stroma	29.2.1.1.1.1.530 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S30A	undefined	Y	C	plastid ribosome	
AT5G24650	1104	AT5G24650.1	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	259	ENV	Ch/E & other	9.6	27.77	100.0	0.0	0.0	60.0	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane	other (e.g. cytoplasm)			envelope	3.0
AT5G24690	1105	AT5G24690.1	similar to RER1 (RETICULATA-RELATED 1) [Arabidopsis thaliana] (TAIR:AT5G22790.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24736.1)	521	ENV	Ch/E/IM	9.14	56.81	96.858018786453 6	0.0	3.1419812135464 4	185.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	3.0
AT5G24870	1106	AT5G24870.1	zinc finger (C3HC4-type RING finger) family protein	520			9.36	56.79	0.0	100.0	0.0	2.0		29.5.11.4.2 protein.degradation.ubiquitin.E3.RING	undefined			-	

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AT5G25510	1107	AT5G25510.1	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative	500	ENV-THY	Ch/E ?	8.9	56.42	50.959095857742 8	0.0	49.040904142257 2	2.0	protein modification	29.4 protein.postranslational modification	chloroplast	Y	C	-	
AT5G25752	1108	AT5G25752.1	rhomboid family protein	280	ENV	Ch/E/IM	9.87	31.59	96.237443394594 1	3.7625566054058 8	0.0	9.0	chaperone and protease	29.5.5 protein.degradation.serine protease	mitochondrion	Y	M	plastid	4.0
AT5G25940	1109	AT5G25940.1	early nodulin-related	115	ENV	Ch/E ?	10.27	12.26	100.0	0.0	0.0	3.0	unknown	33.99 development.unspecified	undefined			-	2.0
AT5G26000	1110	AT5G26000.1	TGG1 (THIOGLUCOSIDE GLUCOHYDROLASE 1); hydrolase, hydrolyzing O-glycosyl compounds	541			5.6	61.13				5.0		16.5.1 secondary metabolism.sulfur-containing.glucosinolates	secreted		S	not plastid	
AT5G26570	1111	AT5G26570.1	PWD (PHOSPHOGLUCAN WATER DIKINASE); catalytic	1196	STR		5.85	131.32	0.0	100.0	0.0	212.0		2.2.2.3 major CHO metabolism.degradation.starch.glucan water dikinase	chloroplast	Y	C	plastid stroma	

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AT5G26742	1112	AT5G26742.1	EMB1138 (EMBRYO DEFECTIVE 1138); ATP binding / ATP-dependent helicase	747	STR-ENV	Ch/E & Ch/S	7.24	81.0	41.004532408141 8	58.995467591858 2	0.0	38.0	RNA Binding ?	27.5* RNA.DEAD/DEAH BOX helicase	chloroplast	Y	C	plastid stroma	
AT5G27240	1113	AT5G27240.1	DNAJ heat shock N-terminal domain-containing protein	1104	ENV-THY	Ch/E ?	9.02	124.44	50.959095857742 8	0.0	49.040904142257 2	2.0	chaperone and protease ?	20.2.1 stress.abiotic.heat	other (e.g. cytoplasm)			-	
AT5G27560	1114	AT5G27560.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO17622.1)	341			4.73	38.04	0.0	100.0	0.0	6.0		35.2 not assigned. unknown	undefined	Y	C	plastid	
AT5G27670	1115	AT5G27670.1	HTA7; DNA binding	150	THY-ENV	other	10.47	15.9	30.888133963744 9	9.6609675714206 2	59.450898464834 5	8.0	DNA binding	28.1.3 DNA.synthesis/chromatin structure. histone	undefined	Y		nucleus	
AT5G28500	1116	AT5G28500.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04550.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65032.1)	434	STR		4.98	48.23	0.0	100.0	0.0	73.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	

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AT5G28540	1117	AT5G28540.1	BIP1; ATP binding	669	ENV-STR	Ch/E ?	5.08	73.63	73.667288366784 5	26.332711633215 5	0.0	15.0	chaperone and protease	29.6 protein.folding	secreted		S	ER	
AT5G28750	1118	AT5G28750.1	thylakoid assembly protein, putative	147	ENV	Ch/E & Ch/Th	9.22	15.71	100.0	0.0	0.0	5.0	protein targeting	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	thylakoid-integral	1.0
AT5G30510	1119	AT5G30510.1	RPS1 (ribosomal protein S1); RNA binding	416	STR	Ch/S	5.12	45.11	8.7940422040316 3	89.392453790626 5	1.8135040053418 8	683.0	translation stroma	29.2.1.1.3.1.1 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S1	chloroplast	Y	C	plastid ribosome	
AT5G33320	1120	AT5G33320.1	CUE1 (CAB UNDEREXPRESSED 1); antiporter / triose-phosphate transmembrane transporter	408	ENV	Ch/E/IM	10.16	44.22	100.0	0.0	0.0	7.0	transporter Pi/PEP	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	6.0
AT5G35100	1121	AT5G35100.1	peptidyl-prolyl cis-trans isomerase	281		Lum	6.82	30.5	0.0	0.0	100.0	4.0		29.6 protein.folding	undefined	Y	C	plastid	
AT5G35170	1122	AT5G35170.1	adenylate kinase family protein	588	THY	Ch/E & Ch/Th	8.84	65.73	14.134471214787 9	11.052194687895 6	74.813334097316 5	24.0	metabolism nucleotide	23.4.1 nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase	chloroplast	Y	C	plastid	

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AT5G35360	1123	AT5G35360.1	CAC2 (acetyl co-enzyme A carboxylase biotin carboxylase subunit)	537	STR	Ch/E & Ch/S	6.84	58.38	8.9984811120858	91.001518887914 2	0.0	162.0	metabolism lipid	11.1.1 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	chloroplast	Y	C	envelope-inner-peripheral-stromal-side	
AT5G35630	1124	AT5G35630.1	GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	430	STR	Ch/S & other	6.42	47.41	11.574736122556 9	87.838998492892 7	0.5862653845504 12	786.0	metabolism carbon	12.2.2 N-metabolism.ammonia metabolism.glutamine synthase	chloroplast	Y	C	plastid stroma	
AT5G35790	1125	AT5G35790.1	G6PD1 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 1); glucose-6-phosphate dehydrogenase	576	STR	Ch/S	7.61	65.42	0.0	90.407850313749 3	9.5921496862506 9	32.0	metabolism carbon	7.1.1 OPP.oxidative PP.G6PD	chloroplast	Y	C	plastid stroma	
AT5G35970	1126	AT5G35970.1	DNA-binding protein, putative	961	STR		7.95	105.04	0.0	100.0	0.0	60.0		28.5* DNA.DEAD BOX helicase	chloroplast	Y	C	plastid stroma	
AT5G36120	1127	AT5G36120.1	YGGT family protein	174			9.89	18.97	0.0	0.0	100.0	6.0		35.2 not assigned. unknown	chloroplast	Y	C	-	2.0
AT5G36170	1128	AT5G36170.1	HCF109 (HIGH CHLOROPHYLL FLUORESCENT 109); translation release factor	456	STR		5.35	50.97	0.0	100.0	0.0	10.0		29.2.5 protein.synthesis.release	undefined	Y	C	plastid	

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AT5G36210	1129	AT5G36210.1	serine-type peptidase	730			5.11	75.21	0.0	100.0	0.0	2.0		29.5 protein.degradation	chloroplast	Y	C	-	
AT5G36700	1130	AT5G36700.1	ATPGLP1/PGLP1 (2-PHOSPHOGLYCOLATE PHOSPHATASE 1); phosphoglycolate phosphatase	362	STR	Ch/S	6.89	39.76	2.8369905331246 8	97.163009466875 3	0.0	269.0	metabolism carbon	1.2.1 PS.photorespiration.phosphoglycolate phosphatase	chloroplast	Y	C	plastid stroma	
AT5G36880	1131	AT5G36880.1	acetyl-CoA synthetase, putative / acetate-CoA ligase, putative	693	STR		5.4	76.73	0.0	100.0	0.0	26.0		11.1.8 lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	chloroplast		C	plastid stroma	
AT5G36890	1132	AT5G36890.1	glycosyl hydrolase family 1 protein	490			5.38	56.07	0.0	100.0	0.0	3.0		26.3 misc.gluco-, galacto- and mannosidases	undefined		M	-	
AT5G37360	1133	AT5G37360.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO38751.1)	309			7.66	33.43	0.0	0.0	100.0	9.0		35.2 not assigned.unknown	chloroplast	Y	C	thylakoid	2.0

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AT5G38410	1134	AT5G38410.1	ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	181	STR-ENV	Ch/S & other	8.21	20.28	18.158276674296 4	76.987621495032 2	4.8541018306714 6	1003.0	metabolism carbon	1.3.2 PS.calvin cyle.rubisco small subunit	chloroplast	Y	C	plastid stroma	
AT5G38430	1135	AT5G38430.1	ribulose bisphosphate carboxylase small chain 1B / RuBisCO small subunit 1B (RBCS-1B) (ATS1B)	181	STR-ENV	Ch/S	7.58	20.28	18.904066413120 4	76.685634564674 4	4.4102990222052 6	851.0	metabolism carbon	1.3.2 PS.calvin cyle.rubisco small subunit	chloroplast	Y	C	plastid stroma	
AT5G38480	1136	AT5G38480.1	GRF3 (GENERAL REGULATORY FACTOR 3); protein phosphorylated amino acid binding	255			4.74	28.6	0.0	100.0	0.0	2.0		30.7 signalling.14-3-3 proteins	other (e.g. cytoplasm)			-	
AT5G38520	1137	AT5G38520.1	hydrolase, alpha/beta fold family protein	362	ENV-THY	Ch/E/IM	6.54	39.57	77.597129628533 2	0.0	22.402870371466 8	16.0	hydrolase ?	35.1 not assigned. no ontology	chloroplast	Y	C	thylakoid	

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AT5G38660	1138	AT5G38660.1	APE1 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT)	286	THY-ENV	Ch/E & Ch/Th	8.6	31.43	20.620968164892 2	0.0	79.379031835107 8	18.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	2.0
AT5G39410	1139	AT5G39410.1	binding / catalytic	454	ENV	Ch & other	8.53	49.68	100.0	0.0	0.0	20.0	metabolism aa Lys	35.2 not assigned. unknown	undefined	Y		-	
AT5G39830	1140	AT5G39830.1	DEG8/DEGP8 (DEGP PROTEASE 8); peptidase/ serine-type peptidase/ trypsin	448	THY	Lum	8.51	47.49	0.0	3.485323 1356739	96.51467 6864326 1	20.0		29.5.5 protein.degradation.serine protease	chloroplast		C	thylakoid-peripheral-lumenal-side	
AT5G40370	1141	AT5G40370.1	glutaredoxin, putative	111			6.71	11.75				2.0		21.4 redox.glutaredoxins	undefined		S	not plastid	
AT5G40410	1142	AT5G40410.1	binding	608			8.71	68.67	0.0	0.0	100.0	1.0		35.1.5 not assigned. no ontology. pentatricopeptide (PPR) repeat-containing protein	undefined		M	-	
AT5G40950	1143	AT5G40950.1	RPL27; structural constituent of ribosome	198	ENV-STR	Ch/S & Ch/Th	9.96	21.73	59.238192612266 4	40.761807387733 6	0.0	17.0	translation stroma	29.2.1.1.1.2.27 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L27	undefined	Y	C	plastid ribosome	

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AT5G41670	1144	AT5G41670.1	6-phosphogluconate dehydrogenase family protein	487	STR		5.62	53.31	0.0	100.0	0.0	103.0		7.1.3 OPP.oxidative PP.6-phosphogluconate dehydrogenase	secreted		S	not plastid	
AT5G41970	1145	AT5G41970.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49320.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62930.1); contains InterPro domain Metal-dependent protein hydrolase (InterPro:IPR003226)	373			5.87	42.3	0.0	100.0	0.0	9.0		35.2 not assigned. unknown	undefined	Y	M	-	
AT5G42070	1146	AT5G42070.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO69519.1)	164	ENV-THY	Ch/E & Ch/Th	8.88	17.68	80.606837168776 6	0.0	19.393162831223 4	7.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	
AT5G42130	1147	AT5G42130.1	mitochondrial substrate carrier family protein	412	ENV	Ch/E/IM	9.37	44.36	98.658363017084 1	1.341636982915 9 2	0.0	24.0	transporter MCF	34.8 transport. metabolite transporters at the envelope membrane	undefined	Y		envelope-inner-integral	3.0

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AT5G42270	1148	AT5G42270.1	VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase	704	THY-ENV	Ch/E & Ch/Th	5.36	75.23	17.097510204805 3	0.0	82.902489795194 8	384.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	thylakoid-integral	
AT5G42390	1149	AT5G42390.1	metalloendopeptidase	1265			6.12	140.6	0.0	100.0	0.0	7.0		29.9* protein.processing	chloroplast	Y	C	plastid stroma	
AT5G42480	1150	AT5G42480.1	ARC6 (ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6)	801	ENV	Ch/E/IM	4.76	88.26	100.0	0.0	0.0	85.0	plastid division	31.2.5 cell.division.plastid	chloroplast	Y	C	envelope-inner	2.0
AT5G42650	1151	AT5G42650.1	AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ oxygen binding	518	ENV-THY	Ch/E & Ch/Th	8.75	58.19	59.086692282514 2	0.0	40.913307717485 8	159.0	metabolism hormone jasmonate	17.7.1.3 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	chloroplast	Y	C	plastoglobules; thylakoid-peripheral-stromal-side	
AT5G42765	1152	AT5G42765.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO61157.1); contains InterPro domain Twin-arginine translocation pathway signal (InterPro: IPR006311)	229			5.94	25.09	0.0	0.0	100.0	4.0		35.2 not assigned. unknown	undefined	Y	C	thylakoid	

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AT5G42960	1153	AT5G42960.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G45170.1); similar to pore protein of 24 kD (OEP24) [Pisum sativum] (GB:CAA04468.1)	213	ENV	Ch/E/OM	9.26	23.41	100.0	0.0	0.0	26.0	transporter ion channel	34.8 transport. metabolite transporters at the envelope membrane	other (e.g. cytoplasm)			envelope -outer	
AT5G43745	1154	AT5G43745.1	phosphotransferase-related	817	ENV	Ch/E/IM	9.14	92.21	98.811351066416 4	0.0	1.1886489335835 6	81.0	transporter ion channel ?	35.1 not assigned. no ontology	undefined	Y	C	-	2.0
AT5G43780	1155	AT5G43780.1	APS4	469	STR		8.88	52.12	0.0	100.0	0.0	24.0		14.1 S-assimilation.APS	chloroplast	Y	C	plastid	
AT5G44316	1156	AT5G44316.1	ATP-binding-cassette transporter, putative	470			5.93	53.08	0.0	100.0	0.0	4.0		35.1 not assigned. no ontology	undefined	Y	C	-	
AT5G44340	1157	AT5G44340.1	TUB4 (tubulin beta-4 chain)	444	STR		4.75	49.82	0.0	100.0	0.0	27.0		31.1 cell.organisation	undefined			-	
AT5G44520	1158	AT5G44520.1	ribose 5-phosphate isomerase-related	296			5.13	32.16	0.0	100.0	0.0	1.0		1.3.10 PS.calvincyle.Rib5P Isomerase	chloroplast	Y	C	-	
AT5G44650	1159	AT5G44650.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO44475.1)	280			4.96	31.81				4.0		35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	1.0
AT5G45170	1160	AT5G45170.1	CbbY protein-related	372	STR		8.02	40.74	0.0	100.0	0.0	61.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	

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AT5G45390	1161	AT5G45390.1	CLPP4 (Clp protease proteolytic subunit 4); endopeptidase Clp	292	STR-ENV	Ch/E & Ch/S	5.37	31.49	45.786112106854 7	54.213887893145 3	0.0	99.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT5G45680	1162	AT5G45680.1	FK506-binding protein 1 (FKBP13)	208		Lum	8.95	22.04	0.0	0.0	100.0	3.0		29.8 protein assembly and cofactor ligation	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT5G45930	1163	AT5G45930.1	CHLI2; magnesium chelatase	418	STR	Ch/S	5.35	46.09	3.7972863790996 1	96.202713620900 4	0.0	203.0	metabolism vitamin and pigment	19.10 tetrapyrrole synthesis.magnesium chelatase	chloroplast	Y	C	plastid	
AT5G46110	1164	AT5G46110.1	APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT); antiporter / triose-phosphate transmembrane transporter	410	ENV-THY	Ch/E/IM	9.75	44.63	78.098043428218 8	0.0	21.901956571781 2	437.0	transporter Pi/TP	34.8 transport.metabolite transporters at the envelope membrane	undefined		M	envelope-inner-integral	8.0
AT5G46290	1165	AT5G46290.1	KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); fatty-acid synthase	473	STR	Ch/E & Ch/S	8.28	50.41	0.0	100.0	0.0	187.0	metabolism lipid	11.1.3 lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	chloroplast	Y	C	plastid stroma	2.0

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AT5G46420	1166	AT5G46420.1	16S rRNA processing protein RimM family	653			5.61	73.78	0.0	100.0	0.0	3.0		29.2.7* protein.synthesis.ribosome biogenesis	chloroplast	Y	C	plastid stroma	
AT5G46580	1167	AT5G46580.1	pentatricopeptide (PPR) repeat-containing protein	711	ENV-STR	Ch/E & Ch/S	8.4	80.88	76.174644552747 2	23.825355447252 8	0.0	6.0	RNA Binding ?	26.54* misc.pentatricopeptide (PPR) repeat-containing protein	chloroplast	Y	C	-	
AT5G47190	1168	AT5G47190.1	ribosomal protein L19 family protein	229	STR-ENV	Ch/S	10.06	25.46	50.120637302424 9	49.879362697575 1	0.0	58.0	translation stroma	29.2.1.1.1.2.19 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L19	chloroplast	Y	C	plastid ribosome	
AT5G47840	1169	AT5G47840.1	AMK2 (ADENOSINE MONOPHOSPHATE KINASE); adenylate kinase	283	STR		7.1	31.45	0.0	87.730280373073 5	12.269719626926 5	25.0		23.4.1 nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase	chloroplast	Y	C	plastid stroma	

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AT5G47860	1170	AT5G47860.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G43540.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68746.1); contains InterPro domain Protein of unknown function DUF1350 (InterPro:IPR010765)	431			8.19	47.78	0.0	100.0	0.0	7.0		35.2 not assigned.unknown	chloroplast	Y	C	-	
AT5G48220	1171	AT5G48220.1	indole-3-glycerol phosphate synthase, putative	379	STR-THY		5.78	41.96	0.0	80.861558905886 6	19.138441094113 4	31.0		13.1.6.5.4 amino acid metabolism.synthesis.aromatic aa.tryptophan.indole-3-glycerol phosphate synthase	undefined	Y	C	plastid stroma	

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AT5G48300	1172	AT5G48300.1	ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE SMALL SUBUNIT 1); glucose-1-phosphate adenylyltransferase	520	STR	Ch/S	6.12	56.65	6.8466814456042 1	93.153318554395 8	0.0	141.0	metabolism carbon	2.1.2.1 major CHO metabolism.synthesis.starch.AGPase	chloroplast	Y	C	plastid stroma	
AT5G48790	1173	AT5G48790.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G73060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49997.1)	316	THY-ENV	Ch/Th	8.12	35.86	20.620968164892 2	0.0	79.379031835107 8	5.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	thylakoid	
AT5G48960	1174	AT5G48960.1	5' nucleotidase family protein	642	STR		5.99	72.89	0.0	100.0	0.0	15.0		23.2 nucleotide metabolism.degradation	undefined	Y	C	plastid stroma	
AT5G49030	1175	AT5G49030.1	OVA2 (OVULE ABORTION 2); ATP binding / aminoacyl-tRNA ligase	1093	STR		6.67	123.0	0.0	100.0	0.0	41.0		29.1.5 protein.aa activation.isoleucine-tRNA ligase	chloroplast	Y	C	plastid stroma	

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AT5G49360	1176	AT5G49360.1	BXL1 (BETA-XYLOSIDASE 1); hydrolase, hydrolyzing O-glycosyl compounds	774			8.79	83.52	0.0	0.0	100.0	8.0		10.6.2 cell wall.degradation. mannan-xylose-arabinose-fucose	secreted		S	-	
AT5G49910	1177	AT5G49910.1	cpHSC70-2 (HEAT SHOCK PROTEIN 70-7); ATP binding / unfolded protein binding	718	STR	Ch/E & Ch/S	5.17	76.99	7.3777777327488 6	92.148884603667 4	0.4733376635836 88	807.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT5G49940	1178	AT5G49940.1	NFU2 (NFU domain protein 2)	235	STR		5.28	25.62	0.0	100.0	0.0	11.0		29.8.1* protein assembly and cofactor ligation.Fe-S assembly	chloroplast	Y	C	plastid stroma	

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AT5G50100	1179	AT5G50100.1	similar to PBng143 [Vigna radiata] (GB:BAB82450.1); contains InterPro domain Thioredoxin-like fold (InterPro: IPR012336); contains InterPro domain Putative thiol-disulphide oxidoreductase DCC (InterPro: IPR007263)	214	ENV	CH/E/IM	9.29	24.43	100.0	0.0	0.0	2.0	redox ?	35.2 not assigned. unknown	mitochondrion	Y	M	-	
AT5G50250	1180	AT5G50250.1	31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative	289	STR		4.9	31.87	0.0	100.0	0.0	37.0		27.1.5* RNA.editing	chloroplast	Y	C	plastid stroma	

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AT5G50920	1181	AT5G50920.1	CLPC (HEAT SHOCK PROTEIN 93-V); ATP binding / ATPase	929	ENV-STR	Ch & other	6.36	103.45	61.473490190711 8	33.295942684533	5.2305671247551 6	2411.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	envelope-inner-peripheral-stromal-side; plastid stroma	
AT5G51010	1182	AT5G51010.1	rubredoxin family protein	154			9.9	17.23	0.0	0.0	100.0	8.0		21.1 redox.thioredoxin	undefined	Y	C	-	1.0
AT5G51020	1183	AT5G51020.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN83158.1); contains InterPro domain Protein of unknown function DUF1001 (InterPro: IPR010404)	269	ENV	Ch/E/OM	6.46	30.33	100.0	0.0	0.0	4.0	plastid division ?	31.2.5 cell.division.plastid	chloroplast		C	envelope-outer	
AT5G51070	1184	AT5G51070.1	ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase	945	STR-ENV	Ch/E & Ch/S	5.89	103.23	41.007379223706 3	52.188519403637 4	6.8041013726563 7	187.0	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma	
AT5G51100	1185	AT5G51100.1	FSD2 (FE SUPEROXIDE DISMUTASE 2); iron superoxide dismutase	305			4.89	34.66	0.0	100.0	0.0	4.0		21.6 redox.dismutases and catalases	chloroplast	Y	C	plastid stroma	

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AT5G51110	1186	AT5G51110.1	similar to dehydratase family [Arabidopsis thaliana] (TAIR:AT1G29810.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62291.1); contains InterPro domain Transcriptional coactivator/pterin dehydratase (InterPro:IPR001533)	220			9.05	23.89	0.0	100.0	0.0	6.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	
AT5G51545	1187	AT5G51545.1	LPA2 (LOW PSII ACCUMULATION2)	185	THY		9.34	20.21	0.0	0.0	100.0	16.0		35.2 not assigned. unknown	undefined	Y	C	thylakoid-integral	
AT5G51690	1188	AT5G51690.1	ACS12 (1-Amino-cyclopropane-1-carboxylate synthase 12); 1-aminocyclopropane-1-carboxylate synthase	495	ENV	Ch/E ?	7.02	55.21	100.0	0.0	0.0	2.0	metabolism hormone ethylene	17.5.1.1 hormone metabolism.ethylene.synthesis-degradation.1-aminocyclopropane-1-carboxylate synthase	undefined		M	-	1.0

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AT5G51720	1189	AT5G51720.1	similar to Os07g0467200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001059590.1); similar to hypothetical protein OsI_025030 [Oryza sativa (indica cultivar-group)] (GB:EAZ03798.1); contains domain PTHR13680 (PTHR13680); contains domain PTHR13680:	108	STR		9.33	11.62	0.0	100.0	0.0	18.0		35.2 not assigned. unknown	undefined			plastid	
AT5G51820	1190	AT5G51820.1	PGM (PHOSPHOGLUCOMUTASE)	623	STR		5.48	67.98	0.0	100.0	0.0	262.0		4.2 glycolysis.PGM	undefined	Y	C	plastid stroma	
AT5G51830	1191	AT5G51830.1	pfkB-type carbohydrate kinase family protein	343	ENV-STR	Ch/E ?	4.99	37.02	51.591112627404 2	48.408887372595 8	0.0	5.0	metabolism carbon	2.2.1.1 major CHO metabolism.degradation.sucrose.fructokinase	other (e.g. cytoplasm)			-	

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AT5G52100	1192	AT5G52100.1	CRR1 (CHLORORESPIRATION REDUCTION 1); dihydrodipicolinate reductase	298			5.88	32.03	0.0	100.0	0.0	6.0		1.1.6.1* PS.lightreaction.NADH DH.assembly	chloroplast	Y	C	plastid stroma	
AT5G52410	1193	AT5G52410.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49433.1); contains InterPro domain S-layer homology region (InterPro:IPR001119)	510	ENV	Ch/E ?	5.29	57.8	100.0	0.0	0.0	10.0	unknown	35.2 not assigned.unknown	chloroplast			-	1.0
AT5G52440	1194	AT5G52440.1	HCF106 (High chlorophyll fluorescence 106)	260	ENV-THY	Ch/E & Ch/Th	8.92	28.23	74.421409276379 6	0.0	25.578590723620 3	20.0	protein targeting	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	thylakoid-integral	1.0
AT5G52520	1195	AT5G52520.1	OVA6/PRORS1 (OVULE ABORTION 6); ATP binding / aminoacyl-tRNA ligase	543	STR		6.55	60.74	0.0	100.0	0.0	91.0		29.1.40 protein.aa activation.bifunctional aminoacyl-tRNA synthetase	undefined	Y	C	mitochondria; plastid stroma	

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AT5G52540	1196	AT5G52540.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G24000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49471.1); contains InterPro domain Protein of unknown function DUF819 (InterPro:IPR008537)	461	ENV	Ch/E/IM	9.96	47.64	96.677210465584	0.0	3.3227895344160 5	29.0	transporter ?	35.2 not assigned. unknown	chloroplast	Y	C	-	9.0
AT5G52780	1197	AT5G52780.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G19100.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49500.1)	168			9.23	18.74	0.0	0.0	100.0	1.0		35.2 not assigned. unknown	undefined	Y	M	-	2.0

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AT5G52920	1198	AT5G52920.1	PKP-BETA1/PKP1/PKP2 (PLASTIDIC PYRUVATE KINASE 1); pyruvate kinase	579	STR		6.56	63.52	0.0	100.0	0.0	91.0		11.1.30 lipid metabolism.FA synthesis and FA elongation.pyruvate kinase	chloroplast	Y	C	plastid stroma	
AT5G52960	1199	AT5G52960.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO69341.1)	170			8.26	19.16	0.0	100.0	0.0	5.0		35.2 not assigned. unknown	chloroplast	Y	C	-	
AT5G52970	1200	AT5G52970.1	thylakoid lumen 15.0 kDa protein	223		Lum	5.66	24.56	0.0	0.0	100.0	1.0		35.1 not assigned. no ontology	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT5G53170	1201	AT5G53170.1	FTSH11 (FtsH protease 11); ATP-dependent peptidase/ ATPase/ metallopeptidase	806	ENV	Ch/E & other	5.8	88.71	100.0	0.0	0.0	95.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	mitochondria; plastid	1.0
AT5G53460	1202	AT5G53460.1	GLT1 (NADH-dependent glutamate synthase 1 gene)	2208	STR		5.97	241.9	0.0	100.0	0.0	178.0		12.2.1.2 N-metabolism.ammonia metabolism.glutamate synthase. NADH dependent	chloroplast	Y	C	plastid	

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AT5G53490	1203	AT5G53490.1	thylakoid lumenal 17.4 kDa protein, chloroplast	236	THY	Ch/Th/Lum	5.97	25.64	14.005875616455 7	10.513576013267 8	75.480548370276 5	83.0	RNA Binding ?	26.54* misc.pentatricopeptide (PPR) repeat-containing protein	undefined	Y	C	thylakoid-peripheral-lumenal-side	1.0
AT5G53580	1204	AT5G53580.1	aldo/keto reductase family protein	365			9.31	40.57	0.0	0.0	100.0	3.0		3.5 minor CHO metabolism.others	undefined	Y		plastid	
AT5G53850	1205	AT5G53850.1	haloacid dehalogenase-like hydrolase family protein	402			5.87	45.02	0.0	100.0	0.0	7.0		3.5 minor CHO metabolism.others	undefined			-	
AT5G53860	1206	AT5G53860.1	EMB2737 (EMBRYO DEFECTIVE 2737)	402	ENV	Ch/E & other	8.57	46.15	100.0	0.0	0.0	15.0	vesicular trafficking ?	35.2 not assigned. unknown	undefined		M	-	
AT5G54190	1207	AT5G54190.1	PORA (Protochlorophyllide reductase A); oxidoreductase/ protochlorophyllide reductase	405	ENV-THY	Ch/E & Ch/Th	9.42	43.86	59.338462682126 7	6.261021306531 8 5	34.400516011341 4	232.0	metabolism vitamin and pigment	19.14 tetrapyrrole synthesis.protochlorophyllide reductase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT5G54270	1208	AT5G54270.1	LHCB3 (LIGHT-HARVESTING CHLOROPHYLL BINDING PROTEIN 3)	265	THY	Ch/Th	4.96	28.7	0.545139968436205	1.875554385849 9 2	97.579305645713 9	381.0	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0

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AT5G54600	1209	AT5G54600.1	50S ribosomal protein L24, chloroplast (CL24)	198	ENV-STR	Ch/S	9.69	21.97	54.746110606496 5	45.253889393503 5	0.0	73.0	translation stroma	29.2.1.1.1.2.24 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L24	chloroplast	Y	C	plastid ribosome	
AT5G54770	1210	AT5G54770.1	THI1 (THIAZOLE REQUIRING)	349	STR		5.81	36.66	0.0	100.0	0.0	154.0		18.2 Co-factor and vitamine metabolism.thiamine	chloroplast	Y	C	mitochondria; plastid stroma	
AT5G54810	1211	AT5G54810.1	TSB1 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT)	470	STR		6.35	50.92	0.0	100.0	0.0	35.0		13.1.6.5.5 amino acid metabolism.synthesis.aromatic aa.tryptophan.tryptophan synthase	chloroplast	Y	C	plastid	
AT5G55220	1212	AT5G55220.1	trigger factor type chaperone family protein	547	STR	Ch/E & Ch/S	5.25	61.73	3.7748695461425 8	96.225130453857 4	0.0	199.0	chaperone and protease	29.6 protein.folding	undefined	Y	C	plastid stroma	
AT5G55280	1213	AT5G55280.1	FTSZ1-1 (FtsZ1-1); structural molecule	433	STR	Ch/E/IM	6.92	45.56	5.7923384239415 6	94.207661576058 4	0.0	57.0	plastid division	31.2.5 cell.division.plastid	chloroplast	Y	C	plastid stroma	
AT5G55510	1214	AT5G55510.1	P-P-bond-hydrolysis-driven protein transmembrane transporter	214	ENV	Ch/E/OM	9.08	22.52	100.0	0.0	0.0	4.0	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane	other (e.g. cytoplasm)			envelope	

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AT5G56000	1215	AT5G56000.1	heat shock protein 81-4 (HSP81-4)	699	STR		4.96	80.14	0.0	100.0	0.0	14.0		20.2.1 stress.abiotic.heat	secreted		S	-	
AT5G56500	1216	AT5G56500.2	ATP binding / protein binding / unfolded protein binding	597	STR	Ch/S	5.73	63.32	15.097306630677 4	82.559303539286 7	2.3433898300358 6	837.0	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT5G56730	1217	AT5G56730.1	peptidase M16 family protein / insulinase family protein	956	ENV	Ch/E	5.4	107.98	100.0	0.0	0.0	3.0	chaperone and protease ?	29.5.7 protein.degradation.metalloprotease	undefined			-	2.0
AT5G57345	1218	AT5G57345.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96592.1)	188			9.19	20.19	0.0	0.0	100.0	9.0		35.2 not assigned. unknown	undefined	Y	C	-	2.0
AT5G57850	1219	AT5G57850.1	aminotransferase class IV family protein	373	STR		8.64	41.06	0.0	100.0	0.0	11.0		26.26.1 misc.aminotransferases.aminotransferase class IV family protein	chloroplast	Y	C	plastid stroma	
AT5G57960	1220	AT5G57960.1	GTP-binding family protein	540			5.75	60.52	0.0	100.0	0.0	1.0		29.2.7* protein.synthesis.ribosome biogenesis	chloroplast	Y	C	plastid stroma	
AT5G58070	1221	AT5G58070.1	lipocalin, putative	186	ENV	Ch/E & other	5.97	21.43	100.0	0.0	0.0	6.0	metabolism lipid / transport ?	11 lipid metabolism	undefined			-	

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AT5G58140	1222	AT5G58140.1	PHOT2 (NON PHOTOTROPIC HYPOCOTYL 1-LIKE); kinase	915	ENV	Ch/E ?	7.04	102.47	100.0	0.0	0.0	5.0	signalling ?	29.4 protein.postranslational modification	undefined		C	-	
AT5G58250	1223	AT5G58250.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN75840.1); contains domain PD020337 (PD020337)	211			7.82	24.1	0.0	0.0	100.0	3.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid	
AT5G58260	1224	AT5G58260.1	Encodes subunit NDH-N of NAD(P)H:plastoquinone dehydrogenase complex (Ndh complex) present in the thylakoid membrane of chloroplasts. This subunit is thought to be required for Ndh complex assembly.	209			9.43	23.39	0.0	0.0	100.0	4.0		1.1.6 PS.lightreaction.NADH DH	undefined	Y	C	thylakoid	

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AT5G58270	1225	AT5G58270.1	STA1 (STARIK1); ATPase, coupled to transmembrane movement of substances	728	ENV	Ch/E & other	9.27	80.42	100.0	0.0	0.0	70.0	transporter ABC	34.16 transport.ABC transporters and multidrug resistance systems	undefined	Y	M	mitochondria	6.0
AT5G58330	1226	AT5G58330.1	malate dehydrogenase (NADP), chloroplast, putative	443	STR	Ch/S & other	5.8	48.31	12.051050807746	87.948949192534	0.0	144.0	metabolism carbon	8.2.99 TCA / org.transformation.other organic acid transformaitons.misc	chloroplast	Y	C	plastid stroma	
AT5G58870	1227	AT5G58870.1	FTSH9 (FtsH protease 9); ATP-dependent peptidase/ ATPase/ metallopeptidase	806	ENV	Ch/E/IM	7.65	87.83	100.0	0.0	0.0	18.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	undefined	Y	C	-	2.0
AT5G59250	1228	AT5G59250.1	sugar transporter family protein	558	ENV	Ch/E/IM	9.02	59.83	100.0	0.0	0.0	88.0	transporter D-xylose-H+ ?	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	11.0
AT5G59750	1229	AT5G59750.1	riboflavin biosynthesis protein, putative	509			5.7	56.14	0.0	100.0	0.0	9.0		18.3.1 Co-factor and vitamine metabolism.riboflavin.GTP cyclohydrolase II	undefined	Y	M	plastid	

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AT5G59870	1230	AT5G59870.1	HTA6; DNA binding	150	THY-ENV	other	10.54	15.96	30.888133963744 9	9.6609675714206 2	59.450898464834 5	7.0	DNA binding	28.1.3 DNA.synthesis/chromatin structure.histone	undefined	Y		nucleus	
AT5G59910	1231	AT5G59910.1	HTB4; DNA binding	150	STR-THY		9.99	16.45	0.0	56.522239153560 8	43.477760846439 2	11.0		28.1.3 DNA.synthesis/chromatin structure.histone	other (e.g. cytoplasm)			nucleus	
AT5G60600	1232	AT5G60600.1	GcpE (CHLOROPLAST BIOGENESIS 4); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	741	STR		6.01	82.25	0.0	100.0	0.0	151.0		16.1.1.6 secondary metabolism.isoprenoids.non-mevalonate pathway.HDS	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT5G60660	1233	AT5G60660.1	PIP2;4/PIP2F (plasma membrane intrinsic protein 2;4); water channel	291	ENV	other	8.21	30.95	100.0	0.0	0.0	2.0	transporter aquaporin	34.19.1 transport.Major Intrinsic Proteins.PIP	other (e.g. cytoplasm)			-	6.0
AT5G60930	1234	AT5G60930.1	chromosome-associated kinesin, putative	1294			6.76	145.22				5.0		31.1 cell.organisation	undefined			-	
AT5G61410	1235	AT5G61410.1	RPE (EMBRYO DEFECTIVE 2728); ribulose-phosphate 3-epimerase	281	STR		8.24	30.0	0.0	96.925502602150 7	3.074497397849 2 5	106.0		1.3.11 PS.calvin cyle.RPE	chloroplast	Y	C	plastid stroma	

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AT5G61790	1236	AT5G61790.1	calnexin 1 (CNX1)	530	ENV	Ch/E ?	4.81	60.48	100.0	0.0	0.0	3.0	vesicular trafficking / signalling calcium ?	30.3 signalling.calcium	secreted		S	-	1.0
AT5G62140	1237	AT5G62140.1	similar to unknown [Populus trichocarpa] (GB:ABK94834.1)	241	ENV	Ch/E/IM	8.85	26.43	100.0	0.0	0.0	7.0	protein targeting ?	35.2 not assigned. unknown	undefined		C	-	
AT5G62720	1238	AT5G62720.1	integral membrane HPP family protein	243	ENV	Ch/E/IM	10.14	25.82	85.924999418780 4	0.0	14.075000581219 6	57.0	transporter ?	35.1 not assigned. no ontology	chloroplast	Y	C	envelope-inner-integral	5.0
AT5G62790	1239	AT5G62790.1	DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE)	477	STR		6.57	51.96	0.0	100.0	0.0	143.0		16.1.1.2 secondary metabolism.isoprenoids.non-mevalonate pathway. DXR	chloroplast	Y	C	plastid stroma	
AT5G63040	1240	AT5G63040.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48460.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64290.1)	366	ENV	Ch/E/IM	9.63	40.66	100.0	0.0	0.0	9.0	unknown	35.2 not assigned. unknown	chloroplast	Y	C	-	5.0
AT5G63050	1241	AT5G63050.1	EMB2759 (EMBRYO DEFECTIVE 2759)	345	ENV	Ch/E ?	9.41	39.29	100.0	0.0	0.0	4.0	unknown	35.2 not assigned. unknown	undefined		M	-	2.0

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AT5G63310	1242	AT5G63310.1	NDPK2 (NUCLEOSIDE DIPHOSPHATE KINASE 2); ATP binding / nucleoside diphosphate kinase	231	STR	Ch/S & other	9.14	25.55	14.086353670223 1	85.913646329776 9	0.0	60.0	metabolism nucleotide	23.4.10 nucleotide metabolism.phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase	chloroplast	Y	C	plastid stroma	
AT5G63420	1243	AT5G63420.1	EMB2746 (EMBRYO DEFECTIVE 2746); catalytic	911			8.42	100.55	0.0	100.0	0.0	8.0		23.2 nucleotide metabolism.degradation	chloroplast	Y	C	plastid stroma	
AT5G63570	1244	AT5G63570.1	GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMINOMUTASE); glutamate-1-semialdehyde 2,1-aminomutase	474	STR	Ch/E & Ch/S	6.42	50.37	6.2230739465009 9	92.778788338848 8	0.998137714650221	437.0	metabolism vitamin and pigment	19.3 tetrapyrrole synthesis.GSA	chloroplast	Y	C	plastid stroma	
AT5G63890	1245	AT5G63890.1	ATHDH (HISTIDINOL DEHYDROGENASE)	452	STR		5.27	48.95	0.0	100.0	0.0	30.0		13.1.7.8 amino acid metabolism.synthesis.histidine.histidinol dehydrogenase	undefined			plastid stroma	

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AT5G63980	1246	AT5G63980.1	SAL1 (FIERY1); 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	407	STR		5.02	37.56	0.0	100.0	0.0	16.0		23.2 nucleotide metabolism.degradation	chloroplast	Y		plastid stroma	
AT5G64040	1247	AT5G64040.1	PSAN (photosystem I reaction center subunit PSI-N); calmodulin binding	171	THY	Ch/Th/Lum	9.11	18.42	4.5497128860162 6	0.0	95.450287113983 7	224.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	undefined	Y	C	thylakoid-peripheral-lumenal-side	
AT5G64050	1248	AT5G64050.1	ATERS/ERS/OVA3 (OVULE ABORTION 3); glutamate-tRNA ligase	570	STR		7.61	63.46	0.0	100.0	0.0	24.0		19.1 tetrapyrrole synthesis.glu-tRNA synthetase	undefined	Y	M	mitochondria; plastid stroma	
AT5G64280	1249	AT5G64280.1	DIT2.2 (DICARBOXYLATE TRANSPORTER 2.2); oxoglutarate:malate antiporter	549	ENV	Ch/E/IM	9.37	58.74	100.0	0.0	0.0	6.0	transporter glutamate/mal	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	-	11.0
AT5G64290	1250	AT5G64290.1	DCT/DIT2.1 (DICARBOXYLATE TRANSPORT); oxoglutarate:malate antiporter	563	ENV-THY	Ch/E/IM	9.33	59.99	76.114364207023 2	0.0	23.885635792976 8	187.0	transporter oxoglut/mal	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope-inner-integral	10.0

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AT5G64300	1251	AT5G64300.1	ATGCH (ARABIDOPSIS THALIANA GTP CYCLOHYDROLASE II); 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	543	STR		5.58	59.05	0.0	100.0	0.0	11.0		18.3.1 Co-factor and vitamine metabolism.riboflavin.GTP cyclohydrolase II	chloroplast	Y	C	plastid	
AT5G64380	1252	AT5G64380.1	fructose-1,6-bisphosphatase family protein	404	STR		6.37	43.97	0.0	100.0	0.0	16.0		1.3.7 PS.calvin cyle.FBPase	undefined	Y	M	plastid	
AT5G64580	1253	AT5G64580.1	AAA-type ATPase family protein	855	ENV	Ch/E/IM	5.66	96.85	100.0	0.0	0.0	52.0	chaperone and protease	29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	-	1.0
AT5G64816	1254	AT5G64816.1	Identical to Uncharacterized protein At5g64816 precursor [Arabidopsis Thaliana] (GB:Q8L8Q8;GB:Q9LV96); similar to unnamed protein product [Vitis vinifera] (GB:CAO22147.1)	130	ENV	Ch/E/IM	8.73	14.44	100.0	0.0	0.0	3.0	unknown	35.2 not assigned.unknown	undefined		C	-	

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AT5G64860	1255	AT5G64860.1	DPE1 (DISPROPORTIONATING ENZYME); 4-alpha-glucanotransferase	576			5.44	64.41	0.0	100.0	0.0	5.0		2.2.2.4 major CHO metabolism.degradation.starch.D enzyme	undefined	Y	C	plastid	
AT5G64940	1256	AT5G64940.1	ATATH13 (ABC2 homolog 13)	761			9.26	86.02	0.0	0.0	100.0	4.0		26.56* misc.ABC1k family	chloroplast	Y	C	envelope-inner-integral	2.0
AT5G65220	1257	AT5G65220.1	ribosomal protein L29 family protein	173	Mix	Ch/S	10.5	19.37	43.550257226806 4	45.972005903643 4	10.477736869550 2	59.0	translation stroma	29.2.1.1.1.2.29 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L29	chloroplast	Y	C	plastid ribosome	
AT5G65250	1258	AT5G65250.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41077.1)	300	ENV	Ch/E/IM	9.93	33.21	96.558379660622 3	0.0	3.441620339377 7 1	28.0	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	2.0
AT5G65350	1259	AT5G65350.1	histone H3	139			11.25	15.59	0.0	39.394425184858 6	60.605574815141 4	4.0		28.1.3 DNA.synthesis/chromatin structure.histone	undefined	Y	C	nucleus	
AT5G65620	1260	AT5G65620.1	peptidase M3 family protein / thimet oligopeptidase family protein	791	STR		5.9	88.75	0.0	100.0	0.0	108.0		29.5.7 protein.degradation.metalloprotease	chloroplast	Y	C	plastid stroma	

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AT5G65840	1261	AT5G65840.1	similar to antioxidant/ oxidoreductase [Arabidopsis thaliana] (TAIR:AT2G37240.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81556.1); contains InterPro domain Thioredoxin-like fold (InterPro: IPR012336); contains InterPro domain Thioredo	275			8.58	29.88	0.0	100.0	0.0	3.0		21 redox	chloroplast	Y	C	plastid stroma	
AT5G66090	1262	AT5G66090.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO23263.1); contains domain Adenine nucleotide alpha hydrolases-like (SSF52402)	210			6.22	22.54	0.0	100.0	0.0	7.0		35.2 not assigned. unknown	chloroplast	Y	C	plastid stroma	

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AT5G66120	1263	AT5G66120.2	3-dehydroquinate synthase, putative	442	STR		7.05	48.06	0.0	100.0	0.0	35.0		18.5 Co-factor and vitamine metabolism.folate & vitamine K	chloroplast	Y	C	plastid	
AT5G66190	1264	AT5G66190.1	ATLFNR1 (LEAF FNR 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transport pathway of ph	360	STR-THY	Ch	8.31	40.32	10.328255498808 6	51.901714999617	37.770029501574 4	523.0	redox	1.1.7 PS.lightreaction.ferredoxin reductase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT5G66530	1265	AT5G66530.1	aldose 1-epimerase family protein	307	STR	Ch/S	5.63	33.69	8.3702689949394 8	91.629731005060 5	0.0	149.0	metabolism carbon	3.5 minor CHO metabolism.others	chloroplast	Y	C	plastid stroma	
AT5G66550	1266	AT5G66550.1	Maf family protein	207			5.35	22.56	0.0	100.0	0.0	6.0		35.1 not assigned. no ontology	undefined		M	plastid	

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AT5G66570	1267	AT5G66570.1	OE33/OEE1/OEE33/PSBO-1/PSBO1 (OXYGEN-EVOLVING ENHANCER 33); oxygen evolving/poly(U) binding	332	THY	Ch/Th/Lum	5.54	35.14	5.5113320298332 3	6.0907410898448 1	88.397926880321 9	625.0	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT5G66720	1268	AT5G66720.1	5-azacytidine resistance protein-related	414			7.6	43.87	0.0	100.0	0.0	3.0		35.1 not assigned.no ontology	chloroplast	Y	C	not plastid	
AT5G67030	1269	AT5G67030.1	ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase	667	ENV	Ch/E/IM	6.6	73.84	74.535588387945 2	13.987621975051 6	11.476789637003 2	48.0	metabolism vitamin and pigment	16.1.4 secondary metabolism.isoprenoids.carotenoids	chloroplast	Y	C	thylakoid	
AtCg00020	1270	AtCg00020	Encodes chlorophyll binding protein D1, a part of the photosystem II reaction center core	353	THY	Ch/Th	5.12	38.93	1.1049807602159 7	0.0	98.895019239784	394.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	

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AtCg00065	1271	AtCg00065	chloroplast gene encoding ribosomal protein s12. The gene is located in three distinct loci on the chloroplast genome and is transplicd to make one transcript.	38	STR-THY	Ch/S	11.57	13.76	8.3367186838527 5	75.617462019152 5	16.045819296994 8	48.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	
AtCg00120	1272	AtCg00120	Encodes the ATPase alpha subunit, which is a subunit of ATP synthase and part of the CF1 portion which catalyzes the conversion of ADP to ATP using the proton motive force. This complex is located in the thylakoid membrane of the chloroplast.	507	THY-ENV	Ch/Th	5.18	55.32	17.601404108971 4	9.6611566799890 1	72.737439211039 5	1599.0	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	other (e.g. cytoplasm)		C	thylakoid-peripheral-stromal-side	

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AtCg00130	1273	AtCg00130	ATPase F subunit.	184	THY	Ch/Th	7.84	21.05	12.124503740628 2	0.0	87.875496259371 8	412.0	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	other (e.g. cytoplasm)		C	thylakoid-integral	
AtCg00140	1274	AtCg00140	ATPase III subunit	81	THY		4.94	7.97	0.0	0.0	100.0	21.0		1.1.4 PS.lightreaction.ATP synthase	secreted		C	thylakoid-integral	
AtCg00150	1275	AtCg00150	Encodes a subunit of ATPase complex CF0, which is a proton channel that supplies the proton motive force to drive ATP synthesis by CF1 portion of the complex.	249	THY		4.96	27.35	0.0	0.0	100.0	27.0		1.1.4 PS.lightreaction.ATP synthase	undefined		C	thylakoid-integral	
AtCg00160	1276	AtCg00160	Chloroplast ribosomal protein S2	236	STR	Ch/S	9.7	26.9	3.9866838117094 7	96.013316188290 5	0.0	92.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	
AtCg00170	1277	AtCg00170	RNA polymerase beta' subunit-2	1376	STR		9.41	156.36	0.0	100.0	0.0	17.0		27.2 RNA.transcription	undefined		C	plastid stroma	
AtCg00180	1278	AtCg00180	RNA polymerase beta' subunit-1	680			8.76	78.58	0.0	100.0	0.0	5.0		27.2 RNA.transcription	undefined		C	plastid stroma	

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AtCg00190	1279	AtCg00190	Chloroplast DNA-dependent RNA polymerase B subunit. The transcription of this gene is regulated by a nuclear encoded RNA polymerase. This gene has been transferred to mitochondrial genome during crucifer evolution.	1072			8.68	121.06	0.0	100.0	0.0	4.0		27.2 RNA.transcription	other (e.g. cytoplasm)		C	plastid stroma	
AtCg00270	1280	AtCg00270	PSII D2 protein	353	THY	Ch/Th	5.45	39.54	2.6392468886666 4	0.0825484590111826	97.278204652322 2	495.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	other (e.g. cytoplasm)		C	thylakoid-integral	
AtCg00280	1281	AtCg00280	chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. promoter contains a blue-light responsive element.	473	THY	Ch/Th	6.7	51.86	1.9158021567611 3	0.0	98.084197843238 9	707.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	

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AtCg00330	1282	AtCg00330	30S chloroplast ribosomal protein S14	100	STR-ENV	Ch/S	11.23	11.74	28.553625377643 5	71.446374622356 5	0.0	32.0	translation stroma	29.2.1.1.1.1.14 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S14	undefined		C	plastid ribosome	
AtCg00340	1283	AtCg00340	Encodes the D1 subunit of photosystem I and II reaction centers.	734	THY-ENV	Ch/Th	6.88	82.47	20.279908940860 5	0.0	79.720091059139 5	378.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	mitochondrion		C	thylakoid-integral	
AtCg00350	1284	AtCg00350	Encodes psaA protein comprising the reaction center for photosystem I along with psaB protein; hydrophobic protein encoded by the chloroplast genome.	750	THY-ENV	Ch/Th	6.6	83.23	15.658437490861	0.0	84.341562509139	514.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	other (e.g. cytoplasm)		C	thylakoid-integral	
AtCg00380	1285	AtCg00380	Chloroplast encoded ribosomal protein S4	201	STR	Ch/S	10.32	23.24	13.684412548871 2	86.315587451128 8	0.0	206.0	translation stroma	29.2.1.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	

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AtCg00420	1286	AtCg00420	Encodes NADH dehydrogenase subunit J. Its transcription is increased upon sulfur depletion.	158			6.5	18.55	0.0	100.0	0.0	6.0		1.1.6 PS.lightreaction.NADH DH	undefined		C	thylakoid	
AtCg00430	1287	AtCg00430	Encodes a protein which was originally thought to be part of photosystem II but its wheat homolog was later shown to encode for subunit K of NADH dehydrogenase.	225			9.17	25.36	0.0	9.7746155337778 4	90.225384466222 2	6.0		1.1.6 PS.lightreaction.NADH DH	undefined		C	thylakoid	
AtCg00470	1288	AtCg00470	ATPase epsilon subunit	132	THY-ENV	Ch/Th	5.83	14.49	20.632332574163 4	2.1510773485131 9	77.216590077323 4	98.0	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	undefined		C	thylakoid-peripheral-stromal-side	
AtCg00480	1289	AtCg00480	chloroplast-encoded gene for beta subunit of ATP synthase	498	THY	Ch/Th & other	5.38	53.93	15.288863589900 3	9.5233558596958	75.187780550403 9	2300.0	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	undefined		C	thylakoid-peripheral-stromal-side	
AtCg00490	1290	AtCg00490	large subunit of RUBISCO.	479	STR-ENV	Ch	5.87	52.95	15.956882558844 5	78.365181110005 9	5.677936331149 5 9	7279.0	metabolism carbon	1.3.1 PS.calvincyle.rubisco large subunit	other (e.g. cytoplasm)		C	plastid stroma	

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AtCg00500	1291	AtCg00500	Encodes the carboxytransferase beta subunit of the Acetyl-CoA carboxylase (ACCase) complex in plastids. This complex catalyzes the carboxylation of acetyl-CoA to produce malonyl-CoA, the first committed step in fatty acid synthesis.	488	ENV	Ch/E/IM	5.89	55.61	95.048148053629 1	3.5763577301140 9	1.3754942162568 1	175.0	metabolism lipid	11.1.1 lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	undefined		C	plastid stroma	

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AtCg00520	1292	AtCg00520	Encodes a protein required for photosystem I assembly and stability. In cyanobacteria, loss of function mutation in this gene increases PSII/PSI ratio without any influence on photoautotrophic growth.	184			9.61	21.4	0.0	0.0	100.0	6.0		29.8 protein assembly and cofactor ligation	undefined		C	plastid stroma	
AtCg00540	1293	AtCg00540	Encodes cytochrome f apoprotein; involved in photosynthetic electron transport chain; encoded by the chloroplast genome and is transcriptionally repressed by a nuclear gene HCF2.	320	THY	Ch/Th	8.34	35.35	11.495751735268 5	0.0	88.504248264731 5	301.0	PS b6-F	1.1.3 PS.lightreaction.cytochrome b6/f	undefined		C	thylakoid-integral	

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AtCg00560	1294	AtCg00560	PSII L protein	38	THY		4.52	4.47	0.0	0.0	100.0	56.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	secreted		C	thylakoid-integral	
AtCg00580	1296	AtCg00580	PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through	83	THY	Ch/Th	4.83	9.39	4.5497128860162 6	0.0	95.4502871139837	160.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	
AtCg00630	1297	AtCg00630	Encodes subunit J of photosystem I.	44			5.87	5.0	0.0	0.0	100.0	9.0		1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	secreted		C	thylakoid-integral	

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AtCg00640	1298	AtCg00640	encodes a chloroplast ribosomal protein L33, a constituent of the large subunit of the ribosomal complex	66			9.78	7.69	0.0	100.0	0.0	9.0		29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
AtCg00650	1299	AtCg00650	chloroplast-encoded ribosomal protein S18	101	ENV-STR	Ch/S	12.16	12.06	51.449313369740 7	37.547871299513 2	11.002815330746 1	40.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	
AtCg00660	1300	AtCg00660	encodes a chloroplast ribosomal protein L20, a constituent of the large subunit of the ribosomal complex	117	ENV-STR	Ch/S	11.89	14.16	57.810045970493 5	42.189954029506 5	0.0	16.0	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined	Y	C	plastid ribosome	

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AtCg00670	1301	AtCg00670	Encodes the only ClpP (caseinolytic protease) encoded within the plastid genome. Contains a highly conserved catalytic triad of Ser-type proteases (Ser-His-Asp). Part of the 350 kDa chloroplast Clp complex. The name reflects nomenclature described i	196	STR-ENV	Ch/E & Ch/S	4.97	22.09	24.226403607846 9	75.773596392153 1	0.0	33.0	chaperone and protease	29.5.5 protein.degradation.serine protease	other (e.g. cytoplasm)		C	plastid stroma; thylakoid-inner-peripheral-stromal-side	
AtCg00680	1302	AtCg00680	encodes for CP47, subunit of the photosystem II reaction center.	508	THY	Ch/Th	6.39	56.03	1.5145108570045	0.0	98.485489142995 5	604.0	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	

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AtCg00710	1303	AtCg00710	Encodes a 8 kD phosphoprotein that is a component of the photosystem II oxygen evolving core. Its exact molecular function has not been determined but it may play a role in mediating electron transfer between the secondary quinone acceptors, QA and Q	73	THY		6.03	7.7	0.0	0.0	100.0	251.0		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	
AtCg00720	1304	AtCg00720	Encodes the cytochrome b(6) subunit of the cytochrome b6f complex.	215	THY	Ch/Th	8.88	24.15	6.2024074425463 9	0.0	93.797592557453 6	195.0	PS b6-F	1.1.3 PS.lightreaction.cytochrome b6/f	other (e.g. cytoplasm)		C	thylakoid-integral	
AtCg00730	1305	AtCg00730	A chloroplast gene encoding subunit IV of the cytochrome b6/f complex	160	THY	Ch/Th	6.55	17.43	4.0847103136494	0.0	95.915289686350 6	159.0	PS b6-F	1.1.3 PS.lightreaction.cytochrome b6/f	other (e.g. cytoplasm)		C	thylakoid-integral	

Accession	pgID	Master Protein	Description (curated)	Length	Localization (SC)	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	ENV SC	STR SC	THY SC	Total SC	Function (putative)	MapMan Bin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AtCg00740	1306	AtCg00740	RNA polymerase alpha subunit	329	STR-THY		7.19	38.13	0.0	59.39135367749	40.60864632251	17.0		27.2 RNA.transcription	undefined		C	plastid stroma	
AtCg00750	1307	AtCg00750	30S chloroplast ribosomal protein S11	138	STR	Ch/S	12.24	15.02	14.907343569686 2	85.092656430313 8	0.0	113.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined	Y	C	plastid ribosome	
AtCg00760	1308	AtCg00760	encodes a chloroplast ribosomal protein L36, a constituent of the large subunit of the ribosomal complex	37	STR-ENV	Ch/S	11.91	4.46	39.003630314089 9	60.996369685910 1	0.0	15.0	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
AtCg00770	1309	AtCg00770	chloroplast 30S ribosomal protein S8	134	STR-ENV	Ch/S	10.93	15.48	20.010853473861 5	63.482624458950 6	16.506522067187 8	115.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	other (e.g. cytoplasm)		C	plastid ribosome	
AtCg00780	1310	AtCg00780	encodes a chloroplast ribosomal protein L14, a constituent of the large subunit of the ribosomal complex	122	STR-THY	Ch/S	9.38	13.58	18.647149534888 8	54.434994364809	26.917856100302 2	75.0	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	

Accession	pgID	Master Protein	Description (curated)	Length	Localization (SC)	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	ENV SC	STR SC	THY SC	Total SC	Function (putative)	MapMan Bin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AtCg00790	1311	AtCg00790	chloroplast gene encoding a ribosomal protein L16, which is a constituent of 50S large ribosomal subunit	135	STR-ENV	Ch/S	11.62	15.29	44.422901794894 4	55.577098205105 6	0.0	34.0	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
AtCg00800	1312	AtCg00800	encodes a chloroplast ribosomal protein S3, a constituent of the small subunit of the ribosomal complex	218	STR-ENV	Ch/S	9.51	25.18	17.615875267341 5	82.384124732658 5	0.0	454.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	
AtCg00810	1313	AtCg00810	encodes a chloroplast ribosomal protein L22, a constituent of the large subunit of the ribosomal complex	160	STR-ENV	Ch/S	9.69	18.58	24.198217551578 4	71.144311795201 1	4.6574706532205 2	65.0	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
AtCg00820	1314	AtCg00820	Encodes a 6.8-kDa protein of the small ribosomal subunit.	92	STR-ENV	Ch/S	10.77	10.57	32.970405234885 8	67.029594765114 2	0.0	23.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	

Accession	pgID	Master Protein	Description (curated)	Length	Localization (SC)	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	ENV SC	STR SC	THY SC	Total SC	Function (putative)	MapMan Bin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AtCg00830	1315	AtCg00830	encodes a chloroplast ribosomal protein L2, a constituent of the large subunit of the ribosomal complex	274	STR-ENV	Ch/S	10.84	29.86	21.212611382823 8	78.787388617176 2	0.0	150.0	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
AtCg00840	1316	AtCg00840	One of two chloroplast genes that encode chloroplast ribosomal protein L23, a constituent of the large subunit of the ribosomal complex	93	STR-ENV	Ch/S	10.65	10.78	21.038133529960 1	78.961866470039 9	0.0	15.0	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
AtCg00860	1317	AtCg00860	Encodes an unknown protein. This gene is regulated by AtSIG6 transcriptionally.	2294	ENV	Ch/S	8.87	269.56	98.073833497928 1	0.0	1.926166502071 8 6	50.0	unknown	29.8 protein assembly and cofactor ligation	undefined		C	plastid stroma	
	1318	ATCG00900.1																	
AtCg01060	1319	AtCg01060	Encodes the PsaC subunit of photosystem I.	81	THY	Ch/Th	6.67	9.03	5.5562794088588 7	0.868926482411396	93.574794108729 7	84.0	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	undefined		C	thylakoid-peripheral-stromal-side	

Accession	pgID	Master Protein	Description (curated)	Length	Localization (SC)	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	ENV SC	STR SC	THY SC	Total SC	Function (putative)	MapMan Bin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AtCg01070	1320	AtCg01070	NADH dehydrogenase ND4L	101	THY		8.73	11.28	0.0	0.0	100.0	10.0		1.1.6 PS.lightreaction.NADH DH	secreted		C	thylakoid-integral	
AtCg01100	1321	AtCg01100	NADH dehydrogenase ND1	360			5.56	40.02	0.0	0.0	100.0	2.0		1.1.6 PS.lightreaction.NADH DH	other (e.g. cytoplasm)		C	thylakoid-integral	
AtCg01110	1322	AtCg01110	Encodes the 49KDa plastid NAD(P)H dehydrogenase subunit H protein. Its transcription is regulated by an ndhF-specific plastid sigma factor, SIG4.	393	STR-THY		5.39	45.5	0.0	53.216880841799 2	46.783119158200 9	49.0		1.1.6 PS.lightreaction.NADH DH	undefined		C	thylakoid	
AtCg01120	1323	AtCg01120	encodes a chloroplast ribosomal protein S15, a constituent of the small subunit of the ribosomal complex	88	Mix	Ch/S	10.81	10.71	38.285198995116 6	47.898272701270 4	13.816528303613	53.0	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	other (e.g. cytoplasm)		C	plastid ribosome	
AtCg01130	1324	AtCg01130	hypothetical protein	1786	ENV	Ch/Th	9.74	213.69	97.569026449317 3	0.0	2.430973550682 8	317.0	unknown	29.8 protein assembly and cofactor ligation	secreted		C	thylakoid-integral	
	1325	AtMg00280																	
	1326	O77727																	

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	1327	P00761																	
	1328	P02533																	
	1329	P02538																	
	1330	P02769																	
	1331	P04259																	
	1332	P04264																	
	1333	P08779																	
	1334	P12035																	
	1335	P13645																	
	1336	P25691																	
	1337	P35527																	
	1338	P35908																	
	1339	P48666																	
	1340	Q28582																	
	1341	Q6EIY9																	
	1342	Q6IMF3																	
	1343	Q6P6Q2																	
	1344	Q6PI71																	
	1345	Q9CPN9																	